

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Murphy, Patricia White, Marga Olson, Sheri Yoshikawa, Matthew Jackson, Geoffrey Eskanderi, Tara Schryer, Brenda Park, Michael
- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 134
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 - (B) STREET: 1111 Pennsylvania Ave., NW
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/084,471
 - (B) FILING DATE: 22 May 1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/055,784
 - (B) FILING DATE: 15 August 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/064,926
 - (B) FILING DATE: 07 November 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/065,367
 - (B) FILING DATE: 12 November 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/071,715
 - (B) FILING DATE: 01 May 1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Michael S. Tuscan
 - (B) REGISTRATION NUMBER: 43,210

RECEIVED
DEC 0 4 2002

TECH CENTER 1600/2900

(C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US	
(ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 202-739-3000	
(B) TELEFAX: 202-739-3001	
(2) INFORMATION FOR SEQ ID NO:1:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE</pre>	
(A) NAME/KEY: exon	
(B) LOCATION: 2675	
(D) OTHER INFORMATION: Exon 5	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
AGGGATTTGC TTTGTTTTAT TTTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTA TTCTT	60 105
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 218 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: exon	
(B) LOCATION: 29210 (D) OTHER INFORMATION: Exon 15	
(D) OTHER INFORMATION: EXOIT 15	
• (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT	
CTGTATCTTG CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC	
CAAGTTCCCT CTGCGTGTTC TCATAAACAG GTATGTGT	218
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 258 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(D) TOPOLOGI. IIMEAL	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

			(D) OT	HER	INFO	RMAT	ION:	Exo	n 16								
		(:	xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	3:						
to go co	gcat gtaa ccto	taaaa aggaa ccaa	aa t aa g tg a	taac ttta	agca tgga aagg	a aa c tg	atgc gaaa	agag agga	tct ata	tttc cagt	agt tgg	ttca ctga	cact _s tggt	ga a gg a	gatt. itggc	aacat atttt tcata aagat	120 180	
			(2) IN	FORM	ATIO	N FO	R SE	Q ID	NO:	4:							
		(:	(A) (B) (C)	LENG TYP: STR	GTH: E: ni ANDE	104: ucle: DNES	ACTE 85 b ic a S: s inea	ase ; cid ingl	pair	s								
				MOLE FEAT		TYP	E: c	DNA										
			(B) LO	CATIO	ON:	Codi 229. RMAT:	10	482		OMI1)						
		(2	xi) :	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	4:						
T A	CTC	CTG(CGC (FGT (CTCG(GACC(GGTG:	IC T	TTTG(TTTT	CGGC(G GTO A GC	GGGT(TTAC'	CGCC ICCG	GCC	GGGA(AAAA	GAA AAG A AT	GCGT(AACT(G CC' t Pro	TGCGCC GAGGGC GCACCT F ATT D Ile	3 120	0
															. CGC Arg		285	5
A															GAA Glu		333	3
															TCT Ser 50		381	L
															CAA Gln		429)
															AAA Lys		477	,
C	'AA	GGG	CTG	ACT	CTG	CCG	CTG	TAC	CAA	TCT	ССТ	GTA	AAA	GAA	TTA	GAT	525	5

(A) NAME/KEY: exon(B) LOCATION: 34...221

Gln	Gly 85	Leu	Thr	Leu	Pro	Leu 90	Tyr	Gln	Ser	Pro	Val 95	Lys	Glu	Leu	Asp		
								AAT Asn								573	
								ATG Met								621	
								AGT Ser 140								669	
								GAT Asp								717	
								AAG Lys								765	
								GTG Val								813	
								CTT Leu								861	
								GTA Val 220								909	
								CAT His								957	
								GAC Asp								1005	
								AAA Lys								1053	
								GGA Gly								1101	
								GTA Val 300								1149	
								AGA Arg								1197	

310	315	320

	ACT Thr 325								1245
	TGT Cys								1293
	GAA Glu								1341
	CAG Gln								1389
	CCG Pro								1437
	GGA Gly 405								1485
	CAA Gln								1533
	AAA Lys								1581
	CCA Pro								1629
	GAT Asp								1677
	AAG Lys 485								1725
	ATC Ile								1773
	AAT Asn								1821
	ACT Thr								1869

											-			AGC Ser		1917
														GGT Gly		1965
														ATA Ile		2013
														AAA Lys 610		2061
														GAA Glu		2109
														TCT Ser		2157
														TCC Ser		2205
														GAA Glu		2253
		AAT	ΔΔΤ	ACA	GTA	ATC	ጥርጥ	CAC	CI N ITT	amm	~ ~ m	ጥለጥ	אאא	CDD	GCA	2301
	Ser				Val									Glu 690		
	TGT	Asn AAT	Asn AAG	Thr 680 GAA	AAA	Ile	Ser CAG	Gln TTA	Asp 685 TTT	Leu ATT	Asp ACC	Tyr CCA	Lys GAA	Glu	Ala GAT	2349
Lys TCT	TGT Cys CTG	Asn AAT Asn TCA	Asn AAG Lys 695 TGC	Thr 680 GAA Glu CTG	AAA Lys CAG	Ile CTA Leu GAA	Ser CAG Gln GGA	Gln TTA Leu 700 CAG	Asp 685 TTT Phe	Leu ATT Ile GAA	ASP ACC Thr	Tyr CCA Pro	GAA Glu 705 CCA	Glu 690 GCT	Ala GAT Asp	
TCT Ser	TGT Cys CTG Leu	AST AST TCA Ser 710	AAG Lys 695 TGC Cys	Thr 680 GAA Glu CTG Leu	AAA Lys CAG Gln	CTA Leu GAA Glu	CAG Gln GGA Gly 715 GAA	TTA Leu 700 CAG Gln	Asp 685 TTT Phe TGT Cys	ATT Ile GAA Glu	ASP ACC Thr AAT ASn GCT	CCA Pro GAT Asp 720 GCA	GAA Glu 705 CCA Pro	Glu 690 GCT Ala AAA	GAT Asp AGC Ser	2349
TCT Ser AAA Lys	TGT Cys CTG Leu AAA Lys 725	ASN AAT ASN TCA Ser 710 GTT Val	Asn AAG Lys 695 TGC Cys TCA Ser	Thr 680 GAA Glu CTG Leu GAT Asp	AAA Lys CAG Gln ATA Ile	CTA Leu GAA Glu AAA Lys 730	CAG Gln GGA Gly 715 GAA Glu	Gln TTA Leu 700 CAG Gln GAG Glu TAC	Asp 685 TTT Phe TGT Cys GTC Val	Leu ATT Ile GAA Glu TTG Leu GAT	ASP ACC Thr AAT Asn GCT Ala 735 ACT	CCA Pro GAT Asp 720 GCA Ala	GAA Glu 705 CCA Pro GCA Ala	Glu 690 GCT Ala AAA Lys	Ala GAT Asp AGC Ser CAC His	2349

ACT Thr	CCT Pro	ACT Thr	TCC Ser	AAG Lys	GAT Asp	GTT Val	CTG Leu	TCA Ser	AAC Asn	CTA Leu	GTC Val	ATG Met	ATT Ile	TCT Ser	AGA Arg	2589
			775					780				GGT	785			2627
Gly	Lys	Glu 790	Ser	Tyr	Lys	Met	Ser 795	Asp	Lys	Leu	Lys	GGT Gly 800	Asn	Asn	Tyr	2637
												GAA Glu				2685
												GAG Glu				2733
												AAG Lys				2781
												CAA Gln				2829
												GAA Glu 880				2877
												AAT Asn				2925
												ACA Thr				2973
												GTT Val				3021
												AAA Lys				3069
												AAG Lys 960				3117
AAA Lys	ATG Met 965	ACT Thr	CTA Leu	GGT Gly	CAA Gln	GAT Asp 970	TTA Leu	AAA Lys	TCG Ser	GAC Asp	ATC Ile 975	TCC Ser	TTG Leu	AAT Asn	ATA Ile	3165
												AAA Lys				3213
CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTC	AGA	ACA	3261

Leu	Leu	Gly		Ile 1000		Asn	His	Ser	Phe 1005	Gly	Gly	Ser		Arg 1010	Thr		
		Asn					Leu	TCT Ser 1020				Ile				3309	
	Met					Ile		GAA Glu			Pro					3357	
Cys	GTT Val 1045	GAA Glu	ATT Ile	GTA Val	Asn	ACC Thr 1050	TTG Leu	GCA Ala	TTA Leu	Asp	AAT Asn 1055	CAA Gln	AAG Lys	AAA Lys	CTG Leu	3405	
				Ser				GTA Val	Ser					Ser		3453	
			Ser					AGT Ser					Gln			3501	
		Lys					Ser	AAC Asn 1100				Thr				3549	
	Ala					Leu		ACT Thr			Glu					3597	
Gln					Gln			AAA Lys		Ser						3645	
				Val				CAG Gln	Met					Thr		3693	
			Cys					CTT Leu 1					Asn			3741	
		Gly					Ser	AAG Lys 180				Gly				3789	
ATT Ile	Lys	CGG Arg 190	AAG Lys	TTT Phe	GCT Ala	Gly	CTG Leu 195	TTG Leu	AAA Lys	AAT Asn	Asp	TGT Cys .200	AAC Asn	AAA Lys	AGT Ser	3837	
GCT Ala 1	TCT Ser 205	GGT Gly	TAT Tyr	TTA Leu	Thr	GAT Asp 210	GAA Glu	AAT Asn	GAA Glu	Val	GGG Gly 215	TTT Phe	AGG Arg	GGC Gly	TTT Phe	3885	
TAT Tyr	TCT Ser	GCT Ala	CAT His	GGC Gly	ACA Thr	AAA Lys	CTG Leu	AAT Asn	GTT Val	TCT Ser	ACT Thr	GAA Glu	GCT Ala	CTG Leu	CAA Gln	3933	

1220		1225		1230	1235	
	Val Lys			G AAT ATT AGT 1 Asn Ile Ser 5		3981
		His Pro Ile		T TCA AGT AAA Ser Ser Lys		4029
Ser Val				CAT AAT GAT His Asn Asp 1280		4077
			Gln Leu Ile	A TTA CAA AAT E Leu Gln Asn 1295		4125
				T ACT GAA AAT Thr Glu Asn 1310		4173
	Glu Asn			GCT GCC AGT Ala Ala Ser		4221
				A AGT AAA AAT Ser Lys Asn		4269
Cys Ile				TTT ACT GAT Phe Thr Asp 1360		4317
			Gln Phe Met	G AAG GAG GGA Lys Glu Gly 1375		4365
				TTG GAA GTT Leu Glu Val 1390		4413
	Ala Cys			AAA GAA CAG Lys Glu Gln		4461
				GAG ACT TCT Glu Thr Ser		4509
Phe Gln				GTC GCC AAA Val Ala Lys 1440		4557
			Asp Gln Lys	CCA GAA GAA Pro Glu Glu 1455		4605

			CAT TCT GAC His Ser Asp 1			4653
	Leu Ser T		ACA GAC ATA Thr Asp Ile 1485			4701
			ACT GGA AAT Thr Gly Asn 1500	Gln Leu Val		4749
Gly Gln		arg Asp Glu	AAG ATC AAA Lys Ile Lys 515			4797
			AAA GTT AAA Lys Val Lys		- · ·	4845
			GAT GAA AAA Asp Glu Lys 1			4893
	Ser Phe S		TGG GCA AAG Trp Ala Lys 1565			4941
_			GCA TGT GAG Ala Cys Glu 1580	Thr Ile Glu		4989
Ala Pro		ys Glu Met	CAG AAT TCT Gln Asn Ser 595			5037
			GTG CCA CCT Val Pro Pro			5085
			CTC AAA ACA Leu Lys Thr 1			5133
		is Glu Asn	GTA GAA AAA Val Glu Lys 1645			5181
			TCC CCT TAT Ser Pro Tyr 1660	Ser Val Ile		5229

Thr	TCA Ser 1685				Ala					Arg						5325
	CAA Gln			Arg					Asp					Tyr		5373
	GAA Glu		Asn					Ile					Lys			5421
	TCC Ser	Glu					Tyr					Ser				5469
	TAT Tyr					Asp					Asp					5517
Ser	AAA Lys 1765				Asp					Pro						5565
	GAT Asp			Asn					Lys					Val		5613
	GCA Ala		Ala					Val					Cys			5661
	CTT Leu	Val					Pro					Asn				5709
	TTG Leu					Ser					Val					5757
Phe	AGG Arg 1845				Gly					Val						5805
	AAA Lys			Asp					Ser					Ile		5853
	AAC Asn		Glu					Ile					Ile			5901
	TGT Cys	Tyr					Asp					Leu				5949
CTA	GAT	AAT	GAT	GAA	TGT	AGC	ACG	CAT	TCA	CAT	AAG	GTT	ттт	GCT	GAC	5997

Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala As 1910 1915 1920	sp
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA T Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Le 1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TG Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Se 1940 1945 1950	er
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TG Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Se 1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CA Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gl 1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA AT Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu II 1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAGT A	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACGU His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Th 2020 2025 2030 2030	r
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AA Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val As 2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Se 2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Ph 2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Ar 2085 2090 2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GA Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Gl 2100 2105 2110 211	u
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Gl	u 5 A 6621

2135	2140	2145
2135	2140	21

	Ile					Tyr					Gln				CAA Gln	6717
	TTG	GTA				AAA	GTC			GTT Val	GAG	AAC			GTT Val	6765
	2165			•		2170					2175				• • • •	
	Gly			Gln					Asn					Ile	GGT Gly 2195	6813
AAA Lys	ACT Thr	GAA Glu	Thr	TTT Phe 2200	TCT Ser	GAT Asp	GTT Val	Pro	GTG Val 2205	AAA Lys	ACA Thr	AAT Asn	Ile	GAA Glu 2210	GTT Val	6861
		Thr					Ser			TAC Tyr		Glu			GCA Ala	6909
	Glu					Phe				GAT Asp	Glu					6957
Lys					Ala					TTT Phe						7005
				Leu					Ile	GGA Gly 2270				Gly		7053
			Leu					Ser		AAA Lys			Leu			7101
		qaA					Asn			AAA Lys		Leu				7149
	Ser					Thr				CGA Arg	Arg					7197
His					Pro					CCC Pro						7245
				Ile					Phe	ACC Thr				Gln		7293
			Lys					Glu		CTG Leu			Glu			7341

TCA Ser	AGC Ser	Asn	TTA Leu 2375	GCA Ala	GTT Val	TCA Ser	Gly	CAT His 2380	CCA Pro	TTT Phe	TAT Tyr	Gln	GTT Val 2385	TCT Ser	GCT Ala	7389
	Arg				ATG Met	Arg					Thr					7437
Lys					CCT Pro					Ser						7485
				Arg	AAT Asn 2425				Glu					Lys		7533
			Gly		GGC Gly			Asp					Ile			7581
		Ile			TTT Phe		Lys					Gln				7629
Val	Thr	Phe 2470	Thr	Lys	TGT Cys	Glu 2	Glu 2475	Glu	Pro	Leu	Asp 2	Leu 2480	Ile	Thr	Ser	7677
Leu	CAG Gln 2485	AAT Asn	GCC Ala	AGA Arg	GAT Asp	ATA Ile 2490	CAG Gln	GAT Asp	ATG Met	Arg	ATT Ile 2495	AAG Lys	AAG Lys	AAA Lys	CAA Gln	7725
				Phe	CCA Pro 2505				Ser					Lys		7773
			Pro		ATC Ile			Lys					Gly			7821
		Ala			CAT His		Gln					Gly				7869
	Cys				AAC Asn	Ser					Ser					7917
Thr					GGT Gly 2					Trp						7965
				Gly	GGA Gly 585				Pro					Lys		8013

			GAA Glu					Leu					Gly			8061
		Leu	ATT Ile 2615				Trp					Tyr				8109
	Trp		CTG Leu			Met					Pro					8157
Asn			CTA Leu		Pro					Leu					_	8205
			GAA Glu	Ile					Arg					Lys		8253
			GAT Asp					Lys					Cys			8301
		Ile	TCA Ser 2695				Asn					Ser				8349
_	Ser		GCA Ala			Gln					Ile					8397
Gly			GCT Ala		Lys					Pro						8445
			GGC Gly	Arg					Gln					His		8493
			GTG Val					Ala					Glu			8541
		Leu	ATG Met 2775				Ser					Arg				8589
	Tyr		AAA Lys			Phe					Arg					8637
Pro			TCG Ser		Phe					Asn						8685
GTA	ATT	ATT	CAA	AGA	GCA	TAC	CCT	ATA	CAG	TGG	ATG	GAG	AAG	ACA	TCA	8733

Val 2820	Ile	Ile	Gln	_	Ala 2825	Tyr	Pro	Ile		Trp 2830	Met	Glu	Lys		Ser 2835	
			TAC Tyr					Glu					Lys			8781
		Tyr	GTG Val 2855				Gln					Ala				8829
	Ile		GAG Glu			Glu					Asn					8877
Tyr			TCA Ser		Ala					Gln						8925
			GAG Glu	Leu					Lys					Pro		8973
			GGT Gly					Glu					Leu			9021
		Gln	ATG Met 2935				Lys					Ile				9069
	Arg		GCC Ala			Ser					Glu					9117
Arg			ACA Thr		Val					Ile						9165
			GAT Asp	Ser					Ile					Ser		9213
			CTG Leu					Lys		_	-		Tyr			9261
		Ser	AAA Lys 3015				Lys					Asn				9309
	Ala		AAA Lys			Gln					Pro					9357
			CAG Gln													9405

3045 3050 3055

				GAG GTG GAC CTA A Glu Val Asp Leu I 30	
		er Val Val Lys		CTT GCC CCT TTC G Leu Ala Pro Phe V 3090	
				ATA AAG TTT TGG A Ile Lys Phe Trp I 3105	
			s Pro His Met	TTA ATT GCT GCA A Leu Ile Ala Ala S 3120	
	Gln Trp Ar		Lys Ser Gly	CTT CTT ACT TTA I Leu Leu Thr Leu F 3135	
				AAA GAG GGC CAC T Lys Glu Gly His F 31	
		n Lys Met Lys		GAG AAT ATT GAC A Glu Asn Ile Asp I 3170	
				ATA CTG CAT GCA A Ile Leu His Ala A 3185	
Asp Pro			Lys Asp Cys	ACT TCA GGG CCG T Thr Ser Gly Pro T 3200	
	Gln Ile Il		Gly Asn Lys	CTT CTG ATG TCT T Leu Leu Met Ser S 3215	
				TCA CTT TGT ATG G Ser Leu Cys Met A 32	
AAA AGG		T TCC ACA CCI		CAG ATG ACT TCA A	
Lys Arg	Lys Ser Va 324		Val Ser Ala 3245	Gln Met Thr Ser L 3250	ys
TCT TGT	324 AAA GGG GA	0 G AAA GAG ATT	3245 GAT GAC CAA		AG 10029

						GTT										10125
	Pro 3285	IIe	Cys	Thr		Val 3290	Ser	Pro	Ala		G1n 3295	Lys	Ala	Phe	GIn	
						ACC Thr									AAA	10173
3300	FIO	Arg	261		3305	TIIL	пуъ	ıyı		3310	PIO	116	пув	-	цув 3315	
						ATG Met										10221
				3320					3325	-1	-2-			3330		
						TCA Ser										10269
			3335					3340					3345		110	
						TCT Ser										10317
		3350					3355			- 1		360	0		110	
						AGG Arg						-				10365
	3365					3370					3375				-1-	
						TGT Cys										10413
3380	J		4	_	3385	-2				3390		-1-			3395	
						GAA Glu										10461
				3400				_	3405	•				3410		
			AAA Lys			ATC Ile	TAA									10485
			3415	-	-											

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

 Met
 Pro
 Ile
 Gly
 Ser
 Lys
 Glu
 Arg
 Pro
 Thr
 Phe
 Phe
 Glu
 Ile
 Phe
 Lys

 Thr
 Arg
 Cys
 Asn
 Lys
 Ala
 Asp
 Leu
 Gly
 Pro
 Ile
 Ser
 Leu
 Asn
 Trp
 Phe

 20
 25
 25
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 30
 3

```
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
                    70
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
                                105
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
        115
                            120
                                                125
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
                        135
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
                    150
                                        155
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
                165
                                   170
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
                               185
Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                           200
                                                205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                       215
                                            220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                   230
                                        235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                245
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
                                265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                            280
Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                       295
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                        315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
               325
                                   330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
           340
                               345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
                                                365
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                       395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
               405
                                   410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
                               425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
       435
                           440
                                               445
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
                                           460
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                   470
                                       475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
```

```
500
                                505
                                                     510
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
                                            540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                        555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                    570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
            580
                                585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                            600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                        615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                    630
                                        635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                645
                                    650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
            660
                                665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
        675
                            680
                                                685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695
                                            700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                    710
                                        715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
                725
                                    730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
                                            780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
            820
                                825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                885
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
            900
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
                                            940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
945
                    950
                                        955
```

```
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
               965
                              970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
           980
                            985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                        1000
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
           1015
                                      1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
       1030
                                   1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
              1045
                                1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
           1060
                            1065
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                         1080
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                     1095
                                       1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
       1110
                         1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
             1125
                               1130 1135
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
          1140
                           1145
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
                         1160
                                           1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                     1175
                                       1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                  1190
                                   1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
              1205
                               1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
          1220
                            1225
                                             1230
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
       1235
                     1240 1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                     1255
                                      1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                 1270
                                   1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
              1285
                                1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
          1300
                            1305
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                        1320
                                          1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                     1335
                                      1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                        1355
       1350
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
              1365
                               1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
                            1385
                                              1390
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
                         1400
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
```

1410		141	.5				1420)			
Asp Thr Phe 1425	Phe Gln	Thr Ala	Ser	Gly	Lys	Asn 1435		Ser	Val	Ala	Lys 1440
Glu Ser Phe	Asn Lys 144		Asn	Phe	Phe 1450		Gln	Lys	Pro	Glu 1455	
Leu His Asn	Phe Ser 1460	Leu Asn	Ser	Glu 1465		His	Ser	Asp	Ile 1470	_	Lys
Asn Lys Met 147		Leu Ser	Tyr 1480		Glu	Thr	Asp	Ile 1485		Lys	His
Lys Ile Leu 1490		149	5		_		1500)			
Thr Phe Gln 1505	_	1510	_	_		1515	5	-			1520
Leu Leu Gly	152	5			1530)				1535	5
Glu Ser Leu	1540			1545	5				1550)	
Thr Ser Glu 155	5		1560)		_		1565	5		•
Tyr Arg Glu 1570		157	5				1580)			
Ile Thr Ala 1585		1590				1595	;				1600
Asp Lys Asn	160	5			1610)			-	1615	5
Ser Asp Asn	1620			1625	;		_		1630)	
Ile Phe Leu 163	5		1640)				1645	i		
Lys Ser Pro 1650		165	5				1660)			
Glu Asn Ser 1665		1670				1675			-		1680
Val Ser Gln	1689	5			1690)				1695	5
Ile Phe Asp	1700			1705					1710)	_
Asn Tyr Leu 171	5		1720)				1725	i		_
Lys Asn His 1730		173	5				1740)			
Met Ser Asn 1745		1750				1755				_	1760
Gly Tyr Leu	1769	5			1770)				1775	i
Lys Asn Val	1780			1785					1790	1	
Asn Val Lys 179	5		1800					1805	;	_	
Cys Val Glu 1810		181	5				1820)			
Ala Ala Ile 1825	Lys Leu	1830	ser	Asn	ser	1835		Pne	GIU	vaı	1840
Pro Pro Ala	Phe Arg 1845		Ser		Lys 1850		Val	Cys	Val	Ser 1855	
Glu Thr Ile	Lys Lys 1860	Val Lys		Ile 1865		Thr	Asp	Ser	Phe 1870		Lys

```
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
       1875 1880 1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                    1895
                                     1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                1910
                                  1915 1920
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
             1925
                              1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
         1940 1945
                                 1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                        1960
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
                     1975
                                     1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arq Gln Val Phe
                 1990
                                  1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
              2005
                              2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
       2020
                 2025
                                            2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
      2035
            2040
                                         2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                    2055
                                      2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                 2070
                                  2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
              2085
                               2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
          2100 2105
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
                       2120
                                         2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                 2135
                                     2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                 2150 2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
              2165
                              2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
          2180
                           2185
                                             2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
                        2200
                                         2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
                    2215
                                     2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                2230
                                  2235
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
             2245
                              2250
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
         2260
                           2265
                                            2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
      2275
              2280
                                        2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
                   2295
                                      2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
                                  2315
                 2310
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
```

	2325		2330		2335	5
Thr Thr Lys Glu 234	_	lu Ile Gln 2349		Asn Phe	Thr Ala 2350	Pro
Gly Gln Glu Phe 2355	Leu Ser Ly	s Ser His 2360	Leu Tyr	Glu His 2365		Leu
Glu Lys Ser Ser 2370		eu Ala Val 875	_	His Pro 2380	Phe Tyr	Gln
Val Ser Ala Thr 2385	Arg Asn Gl 2390	u Lys Met	Arg His 2395	Leu Ile	Thr Thr	Gly 2400
Arg Pro Thr Lys	Val Phe Va 2405	al Pro Pro	Phe Lys 2410	Thr Lys	Ser His	
His Arg Val Glu 242	0	2425	5		2430	_
Gln Lys Gln Asn 2435	Ile Asp Gl	y His Gly 2440	Ser Asp	Asp Ser 2445		Lys
Ile Asn Asp Asn 2450		s Gln Phe	_	Asn Asn 2460	Ser Asn	Gln
Ala Ala Ala Val 2465	Thr Phe Th	r Lys Cys	Glu Glu 6 2475	Glu Pro	Leu Asp	Leu 2480
Ile Thr Ser Leu	Gln Asn Al 2485	a Arg Asp	Ile Gln 2 2490	Asp Met	Arg Ile 2495	_
Lys Lys Gln Arg 250	_	al Phe Pro 2505		Gly Ser	Leu Tyr 2510	Leu
Ala Lys Thr Ser 2515	Thr Leu Pr	o Arg Ile 2520	Ser Leu	Lys Ala 2525		Gly
Gly Gln Val Pro 2530		s Ser His	-	Leu Tyr 2540	Thr Tyr	Gly
Val Ser Lys His 2545	Cys Ile Ly 2550	s Ile Asn	Ser Lys 2 2555	Asn Ala	Glu Ser	Phe 2560
~ 7 - 1 1 1					_	
Gln Phe His Thr	Glu Asp Ty 2565	r Phe Gly	Lys Glu : 2570	Ser Leu	Trp Thr 2575	_
Lys Gly Ile Gln 258	2565 Leu Ala As	_	2570 Trp Leu	Ile Pro	2575	5
Lys Gly Ile Gln	2565 Leu Ala As 0	p Gly Gly 2585	2570 Trp Leu :	Ile Pro	2575 Ser Asn 2590 Asp Thr	Asp
Lys Gly Ile Gln 258 Gly Lys Ala Gly	2565 Leu Ala As O Lys Glu Gl Lys Leu Il	sp Gly Gly 2585 u Phe Tyr 2600	2570 Trp Leu : 5 Arg Ala :	Ile Pro Leu Cys 2605	2575 Ser Asn 2590 Asp Thr	Asp Pro
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro	2565 Leu Ala As 0 Lys Glu Gl Lys Leu Il 26	sp Gly Gly 2585 u Phe Tyr 2600 e Ser Arg	2570 Trp Leu : 5 Arg Ala :	Ile Pro Leu Cys 2605 Val Tyr 2620	2575 Ser Asn 2590 Asp Thr	Asp Pro Tyr
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630	sp Gly Gly 2585 The Tyr 2600 The Ser Arg 515 The Ala Ala	2570 Trp Leu : 5 Arg Ala : Ile Trp : Met Glu (Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala	2575 Ser Asn 2590 Asp Thr Asn His	Asp Pro Tyr Lys 2640 Leu
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl	sp Gly Gly 2585 Tu Phe Tyr 2600 The Ser Arg 515 The Ala Ala The Ser Pro	2570 Trp Leu: 5 Arg Ala: Ile Trp: Met Glu: 2635 Glu Arg: 2650 Arg Ser:	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655	Asp Pro Tyr Lys 2640 Leu
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl	sp Gly Gly 2585 .u Phe Tyr 2600 .e Ser Arg 515 .u Ala Ala .u Ser Pro .u Ile Asp 2665	Trp Leu : Arg Ala : Ile Trp : Met Glu : 2635 Glu Arg : 2650 Arg Ser :	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val	Asp Pro Tyr Lys 2640 Leu Ile
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr 2666 Lys Lys Ile Met	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl Glu Arg As Ile Ile Se	sp Gly Gly 2585 u Phe Tyr 2600 e Ser Arg 515 u Ala Ala u Ser Pro u Ile Asp 2665 p Asp Thr 2680	2570 Trp Leu : Arg Ala : Ile Trp : Met Glu : 2635 Glu Arg : 2650 Arg Ser : Ala Ala : Ala Asn :	Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg Lys Thr 2685	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val	Asp Pro Tyr Lys 2640 Leu Ile Leu
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr 2666 Lys Lys Ile Met 2675 Cys Val Ser Asp	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl Glu Arg As Ile Ile Se	sp Gly Gly 2585 au Phe Tyr 2600 ae Ser Arg 515 au Ala Ala au Ser Pro au Ile Asp 2665 ap Asp Thr 2680 ar Leu Ser	2570 Trp Leu : Arg Ala : Ile Trp : Met Glu : 2635 Glu Arg : 2650 Arg Ser : Ala Ala : Ala Asn :	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg Lys Thr 2685 Ile Ser	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val	Asp Pro Tyr Lys 2640 Leu Ile Leu Ser
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr 266 Lys Lys Ile Met 2675 Cys Val Ser Asp 2690 Ser Asn Lys Thr	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl Glu Arg As Ile Ile Se Ser Ser Al 2710	sp Gly Gly 2585 au Phe Tyr 2600 ae Ser Arg 515 au Ala Ala au Ser Pro au Ile Asp 2665 ap Asp Thr 2680 ar Leu Ser 55 a Asp Thr	2570 Trp Leu : Arg Ala : Ile Trp : Met Glu : 2635 Glu Arg : 2650 Arg Ser : Ala Ala : Ala Asn : Gln Lys : 2715	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg Lys Thr 2685 Ile Ser 2700 Val Ala	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val Glu Thr Ile Ile	Asp Pro Tyr Lys 2640 Leu Ile Leu Ser Glu 2720 Leu
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr 266 Lys Lys Ile Met 2675 Cys Val Ser Asp 2690 Ser Asn Lys Thr	2565 Leu Ala As Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl Glu Arg As Ile Ile Se Ser Ser Al 2710 Trp Tyr Al 2725 Lys Asn Gl	sp Gly Gly 2585 au Phe Tyr 2600 ae Ser Arg 55 au Ala Ala au Ser Pro au Ile Asp 2665 ap Asp Thr 2680 ar Leu Ser 595 a Asp Thr	2570 Trp Leu Arg Ala Ile Trp Met Glu 2635 Glu Arg 2650 Arg Ser Ala Ala Ala Asn Gln Lys 2715 Ala Gln 1 2730 Thr Val	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg Lys Thr 2685 Ile Ser 2700 Val Ala Leu Asp	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val Glu Thr Ile Ile Pro Pro 2735	Asp Pro Tyr Lys 2640 Leu Ile Leu Ser Glu 2720 Leu
Lys Gly Ile Gln 258 Gly Lys Ala Gly 2595 Gly Val Asp Pro 2610 Arg Trp Ile Ile 2625 Glu Phe Ala Asn Lys Tyr Arg Tyr 266 Lys Lys Ile Met 2675 Cys Val Ser Asp 2690 Ser Asn Lys Thr 2705 Leu Thr Asp Gly Leu Ala Val Leu	Lys Glu Gl Lys Glu Gl Lys Leu Il 26 Trp Lys Le 2630 Arg Cys Le 2645 Asp Thr Gl Glu Arg As Ile Ile Se Ser Ser Al 2710 Trp Tyr Al 2725 Lys Asn Gl	sp Gly Gly 2585 au Phe Tyr 2600 ae Ser Arg 515 au Ala Ala au Ser Pro au Ile Asp 2665 ap Asp Thr 2680 ar Leu Ser 595 a Asp Thr a Val Lys ay Arg Leu 2745	Trp Leu Arg Ala Ile Trp Met Glu 2635 Glu Arg 2650 Arg Ser Ala Ala Ala Asn Gln Lys 2715 Ala Gln 2730 Thr Val 6	Ile Pro Leu Cys 2605 Val Tyr 2620 Cys Ala Val Leu Arg Arg Lys Thr 2685 Ile Ser 2700 Val Ala Leu Asp Gly Gln	2575 Ser Asn 2590 Asp Thr Asn His Phe Pro Leu Gln 2655 Ser Ala 2670 Leu Val Glu Thr Ile Ile Pro Pro 2735 Lys Ile 2750 Thr Pro	Asp Pro Tyr Lys 2640 Leu Ile Leu Ser Glu 2720 Leu Ile

```
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
2785
                  2790
                                     2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
              2805
                                2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
          2820
                             2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
              2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
   2850
                     2855
                                        2860
Leu Phe Thr Lys Ile Glu Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                  2870
                                     2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
              2885
                                 2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
           2900
                             2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
                        2920
                                            2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                     2935
                              2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
                                    2955
                  2950
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
              2965
                                2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
           2980
                             2985
                                                2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
                         3000
                                            3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                     3015
                                        3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                                     3035
                  3030
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
              3045 3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
           3060
                             3065
                                              3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
                         3080
                                            3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
                      3095
                                        3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
                  3110
                                     3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
              3125
                                 3130
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
           3140
                             3145
                                                3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
                                 3165
      3155
                      3160
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
                                       3180
                     3175
   3170
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
                 3190
                                    3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
              3205
                                 3210
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
                             3225
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
```

		3235	5				3240)				324	5			
Thr	Ser 3250		Ser	Cys	Lys	Gly 325	Glu		Glu	Ile	Asp 3260	Asp	Gln	Lys	Asn	
3265	5				3270)				3275	5		Pro		3280	
Pro	Pro	Val	Ser	Pro 3285		Cys	Thr	Phe	Val 3290		Pro	Ala	Ala	Gln 3295	_	
			3300)				3305	5	_	_		Thr 3310)		
		3315	5				3320)				3325				
	3330)				3335	5				3340)	Glu			
Ala 3345		Ile	Asn	Thr	Gln 3350		Leu	Leu	Ser	Gly 3355		Thr	Gly	Glu	Lys 3360	
Gln	Phe	Ile	Ser	Val 3365		Glu	Ser	Thr	Arg 3370		Ala	Pro	Thr	Ser 3375		
			3380	ŀ				3385	5				Leu 3390)	_	
		3395	;				3400)		Glu	Cys	Glu 3405	Lys	Asn	Lys	
Gln	Asp 3410		Ile	Thr		Lys 3415		Tyr	Ile							
		(2)	INF	ORMA	TION	FOF	SEÇ) ID	NO:6	i :						
	(i	(A) (B) (C) (D) i) M x) F	QUEN LENG TYPE STRA TOPO OLEC EATU	TH: : nu NDED LOGY ULE RE:	1048 clei NESS : li TYPE	5 ba c ac : dc near	se p id uble	airs								
			NAM LOC						ce							
		(D)	OTH	ER I	NFOR	MATI	ON:	BRCA	.2 (0	MI2)						
	(i	(A) (B)	EATU NAM LOC OTH 113	E/KE ATIO	N: 3 NFOR	624 MATI			A or	G.	Xaa	(ami	no a	cid	positio	n
	(x	i) S	EQUE	NCE :	DESC	RIPT	ION:	SEQ	ID	NO : 6	:					
TCTG ACAG	CTGC ATTT	GC C GT G	TCGG ACCG	GTGT GCGC	C TT G GT	TTGC TTTT	GGCG GTCA	GTG GCT	GGTC TACT	GCC CCG	GCCG GCCA	GGAG AAAA	AA G AG A ATG	CGTG ACTG CCT	GCGCC AGGGG CACCT ATT Ile	120 180 237

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC

Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys

				TTA Leu												333	
				CCA Pro 40												381	
_				AAT Asn												429	
				AAT Asn												477	
				CTG Leu												525	
				GAC Asp												573	
				GTG Val 120												621	
				AAT Asn												669	
				ACA Thr												717	
				CCA Pro												765	
				CTA Leu												813	
				ACA Thr 200												861	
				GCA Ala												909	
				TAT Tyr												957	
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005	

Asp	Arg 245	Phe	Ile	Ala	Ser	Val 250	Thr	Asp	Ser	Glu	Asn 255	Thr	Asn	Gln	Arg	
GAA Glu 260	GCT Ala	GCA Ala	AGT Ser	CAT His	GGA Gly 265	TTT Phe	GGA Gly	AAA Lys	ACA Thr	TCA Ser 270	GGG Gly	AAT Asn	TCA Ser	TTT Phe	AAA Lys 275	1053
					GAC Asp											1101
					GAA Glu											1149
					TCT Ser											1197
					AGG Arg											1245
					AAA Lys 345											1293
					AAT Asn											1341
					GAG Glu											1389
					TGT Cys											1437
AAT Asn	GGA Gly 405	GCC Ala	CAG Gln	ATG Met	GAG Glu	AAA Lys 410	ATA Ile	CCC Pro	CTA Leu	TTG Leu	CAT His 415	ATT Ile	TCT Ser	TCA Ser	TGT Cys	1485
GAC Asp 420	CAA Gln	AAT Asn	ATT Ile	TCA Ser	GAA Glu 425	AAA Lys	GAC Asp	CTA Leu	TTA Leu	GAC Asp 430	ACA Thr	GAG Glu	AAC Asn	AAA Lys	AGA Arg 435	1533
					ACT Thr											1581
					AAG Lys											1629
AGA Arg	GAT Asp	GAA Glu	GAG Glu	CAG Gln	CAT His	CTT Leu	GAA Glu	TCT Ser	CAT His	ACA Thr	GAC Asp	TGC Cys	ATT Ile	CTT Leu	GCA Ala	1677

		470			475			480		
	AAG Lys 485									1725
	ATC Ile									1773
	AAT Asn									1821
	ACT Thr									1869
	AAG Lys									1917
	GCC Ala 565									1965
	TCC Ser									2013
	GAA Glu									2061
	CTA Leu									2109
	CTT Leu									2157
	AGA Arg 645									2205
1	AGC Ser									2253
	TCT Ser									2301

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT

Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp

TCT Ser	CTG Leu	TCA Ser 710	Cys	CTG Leu	CAG Gln	GAA Glu	GGA Gly 715	CAG Gln	TGT Cys	GAA Glu	AAT Asn	GAT Asp 720	CCA Pro	AAA Lys	AGC Ser	2397
AAA Lys	AAA Lys 725	GTT Val	TCA Ser	GAT Asp	ATA Ile	AAA Lys 730	GAA Glu	GAG Glu	GTC Val	TTG Leu	GCT Ala 735	GCA Ala	GCA Ala	TGT Cys	CAC His	2445
											ACT Thr					2493
											AGC Ser					2541
											GTC Val					2589
											AAA Lys					2637
GAA Glu	TCT Ser 805	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr 810	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met 815	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
GAT Asp 820	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn 825	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn 830	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro 835	2733
											AGA Arg					. 2781
											AAT Asn					2829
ACT Thr	TCA Ser	ATT Ile 870	TCA Ser	AAA Lys	ATA Ile	ACT Thr	GTC Val 875	AAT Asn	CCA Pro	GAC Asp	TCT Ser	GAA Glu 880	GAA Glu	CTT Leu	TTC Phe	2877
											GCT Ala 895					2925
											GAA Glu					2973
											ATG Met					3021

	ACA Thr															3069
	TAT Tyr															3117
	ATG Met 965															3165
	AAA Lys															3213
	TTA Leu		Pro					Ser					Phe			3261
Ala	TCA Ser	Asn 1	Lys 1015	Glu	Ile	Lys	Leu 1	Ser 1020	Glu	His	Asn	Ile	Lys 1025	Lys	Ser	3309
Lys		Phe 1030	Phe	Lys	Asp	Ile	Glu 1035	Glu	Gln	Tyr	Pro	Thr 1040	Ser	Leu	Ala	3357
Cys	GTT Val 1045				Asn					Asp						3405
	AAG Lys			Ser					Ser					Ser		3453
	GTT Val		Ser					Ser					Gln			3501
	TCC Ser	Lys					Ser					Thr				3549
	GCA Ala					Leu					Glu					3597
Gln	TTT Phe 1125				Gln					Ser						3645
	ACA Thr			Val					Met					Thr		3693
TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741

Ser	Glu	Glu	-	Arg 1160	Asp	Ala	Asp		His L165	Val	Ile	Met		Ala 1170	Pro	
		Gly					Ser				GAA Glu	Gly				3789
	Lys					Gly					GAC Asp					3837
Ala					Thr					Val	GGG Gly 1215					3885
				Gly					Val		ACT Thr			Leu		3933
			Lys					Ile			ATT Ile		Glu			3981
		Glu					Ser				AGT Ser	Lys				4029
	Val					Lys					AAT Asn					4077
Ser					Lys					Leu	CAA Gln 1295					4125
				Thr					Ile		GAA Glu			Lys		4173
			Asn					Tyr			GCC Ala		Arg			4221
		Leu					Ser				AAA Lys	Asn				4269
	Ile					Thr					ACT Thr					4317
Ile										Lys	GAG Glu					4365
	1365				:	L370				-	1375					

1380		1385	1390		1395
		s Gly Asn Thr		GAA CAG TTA ACT Glu Gln Leu Thr 1410	
				ACT TCT GAT ACA Thr Ser Asp Thr 1425	
			ı Ile Ser Val	GCC AAA GAG TCA Ala Lys Glu Ser 1440	
	s Ile Val Ası		Gln Lys Pro	GAA GAA TTG CAT Glu Glu Leu His 1455	
				AGA AAG AAC AAA Arg Lys Asn Lys	
		Glu Glu Thr		AAA CAC AAA ATA Lys His Lys Ile 1490	
				CTA GTG ACC TTC Leu Val Thr Phe 1505	
			lle Lys Glu	CCT ACT CTG TTG Pro Thr Leu Leu 1520	
	s Thr Ala Sei		Val Lys Ile	GCA AAG GAA TCT Ala Lys Glu Ser 1535	
				CAA GGT ACT AGT Gln Gly Thr Ser	
		His Gln Trp		CTA AAG TAC AGA Leu Lys Tyr Arg 1570	
		ı Glu Leu Ala		ATT GAG ATC ACA Ile Glu Ile Thr 1585	
			Asn Ser Leu	AAT AAT GAT AAA Asn Asn Asp Lys 1600	
	l Ser Ile Glu		Pro Pro Lys	CTC TTA AGT GAT Leu Leu Ser Asp 1615	

					AAA AGT ATO Lys Ser Ile		5133
		s Glu Ası			ACA GCA AAA Thr Ala Lys		5181
	hr Cys			Tyr Ser	GTC ATT GAA Val Ile Glu 1665	ı Asn Ser	5229
_	_				ACT TCT GTO Thr Ser Val		5277
	er Leu		s Lys Trp	Leu Arg	GAA GGA ATA Glu Gly Ile 1695		5325
					GTA GGA AAT Val Gly Asr		5373
		r Asn Se			AAT GAC AAA Asn Asp Lys		5421
	er Glu			Ser Asn	AGT AGC ATO Ser Ser Met 1745	Ser Asn	5469
					GAT TCA GGA Asp Ser Gly 1760		5517
	ys Asn		Gly Ile	Glu Pro	GTA TTG AAG Val Leu Lys 1775		5565
					ATA TCC AAT		5613
		r Pro Gli			GAT ATT TGO Asp Ile Cys		5661
	eu Val	 		Lys Asn	AAA AAT GCA Lys Asn Ala 1825	Ala Ile	5709
					GTA GGG CCA Val Gly Pro 1840		5757

	GG ATA rg Ile 45			Gly					Val						5805
	AA GTG ys Val		Asp					Ser					Ile		5853
	AC AAC sn Asn	Glu					Ile					Ile			5901
	GT TAC ys Tyr					Asp					Leu				5949
	AT AAT sp Asn 1910				Ser					Lys					5997
	AG AGT ln Ser 25			Ile					Gln						6045
	AA GTT ys Val		Lys					Asp					Thr		6093
	TA TGT le Cys	Lys					Lys					Val			6141
	AT ACT sn Thr					Ser					Lys				6189
_	CA GAT er Asp 1990				Gln					Val					6237
	AT AGT sp Ser 05			Gln					Val						6285
	AT TCA is Ser		Gln					Glu					Arg		6333
	AA CAT lu His	Leu					Gly					Val			6381
	CT GCT er Ala					Ser					Lys				6429
ATT T	TA GAA	AGT	TCC	TTA	CAC	AAA	GTT	AAG	GGA	GTG	TTA	GAG	GAA	TTT	6477

Ile		Glu 2070	Ser	Ser	Leu		Lys 2075	Val	Lys	Gly		Leu 2080	Glu	Glu	Phe	
Asp		ATC Ile			Glu					Tyr						6525
		GTA Val		Lys					Val					Pro		6573
		GTA Val	Asn					Lys					Glu			6621
		AAT Asn					Glu					Glu				6669
	Ile	AAA Lys 2150				Tyr					Gln		-		_	6717
Gln		GTA Val			Thr					Val						6765
		AAA Lys		Gln					Asn					Ile		6813
				-	100				2	2190				2	2195	
		GAA Glu	Thr	TTT	TCT			Pro	GTG	AAA			Ile	GAA	GTT	6861
Lys TGT	Thr	Glu ACT Thr	Thr Z TAC	TTT Phe 2200	TCT Ser	Asp GAT	Val TCA Ser	Pro Z GAA	GTG Val 2205	AAA Lys TAC	Thr	Asn GAA Glu	Ile Z ACA	GAA Glu 2210 GAA	GTT Val	6861
TGT Cys GTA	Thr TCT Ser GAA Glu	Glu ACT Thr	Thr TAC Tyr 215 GCT	TTT Phe 2200 TCC Ser	TCT Ser AAA Lys GCT	Asp GAT Asp TTT Phe	Val TCA Ser 2	GAA Glu 2220 GAA	GTG Val 2205 AAC Asn	AAA Lys TAC Tyr	Thr TTT Phe GAA Glu	Asn GAA Glu CTG	ACA Thr 2225	GAA Glu 2210 GAA Glu	GTT Val GCA Ala	
TGT Cys GTA Val	Thr TCT Ser GAA Glu CTG	Glu ACT Thr ATT Ile	Thr TAC Tyr 215 GCT Ala	TTT Phe 2200 TCC Ser AAA Lys	TCT Ser AAA Lys GCT Ala	Asp GAT Asp TTT Phe ACA	TCA Ser ATG Met 2235	GAA Glu 2220 GAA Glu	GTG Val 2205 AAC Asn GAT Asp	AAA Lys TAC Tyr GAT Asp	Thr TTT Phe GAA Glu ACA	GAA Glu CTG Leu 2240	ACA Thr 2225 ACA Thr	GAA Glu 2210 GAA Glu GAT Asp	GTT Val GCA Ala TCT Ser	6909
TGT Cys GTA Val	Thr TCT Ser GAA Glu 2 CTG Leu 2245	ACT Thr 2 ATT Ile 2230 CCA	TAC TYP 2215 GCT Ala AGT Ser	TTT Phe 2200 TCC Ser AAA Lys CAT His	TCT Ser AAA Lys GCT Ala GCC Ala	GAT Asp TTT Phe ACA Thr 2250	TCA Ser ATG Met 235 CAT His	GAA Glu 2220 GAA Glu TCT Ser	GTG Val 2205 AAC Asn GAT Asp CTT Leu	AAA Lys TAC Tyr GAT Asp	Thr TTT Phe GAA Glu ACA Thr 2255	GAA Glu CTG Leu 2240 TGT Cys	ACA Thr 2225 ACA Thr CCC Pro	GAA Glu 2210 GAA Glu GAT Asp GAA Glu	GCA Ala TCT Ser AAT Asn	6909 6957
Lys TGT Cys GTA Val AAA Lys GAG Glu 2260	Thr TCT Ser GAA Glu 2 CTG Leu 2245 GAA Glu CTT	ACT Thr 2 ATT Ile 2230 CCA Pro	TAC TYC 215 GCT Ala AGT Ser GTT Val TTA Leu	TTT Phe 2200 TCC Ser AAA Lys CAT His	TCT Ser AAA Lys GCT Ala GCC Ala TCA Ser 2265	GAT Asp TTT Phe ACA Thr 2250 AAT Asn	TCA Ser ATG Met 2235 CAT His	GAA Glu 2220 GAA Glu TCT Ser AGA Arg	GTG Val 2205 AAC Asn GAT Asp CTT Leu ATT Ile	AAA Lys TAC Tyr GAT Asp TTT Phe 2 GGA Gly 2270	Thr TTT Phe GAA Glu 2 ACA Thr 2255 AAA Lys	GAA Glu CTG Leu 2240 TGT Cys AGA Arg	ACA Thr 2225 ACA Thr CCC Pro AGA Arg	GAA Glu 2210 GAA Glu GAT Asp GAA Glu	GTT Val GCA Ala TCT Ser AAT Asn GAG Glu 2275	6909 6957 7005

2295	2300	2305
	2300	2303

											AGA					7197
гуѕ		Tnr 2310	Pro	Asp	GIY			Lys	Asp	Arg	Arg		Phe	Met	His	
		2310					2315					2320				
CAT	GTT	TCT	TTA	GAG	CCG	АТТ	ACC	ፐርጥ	СΤΆ	כככ	TTT	CGC	ልሮአ	አ ርጥ	እ እ C	7245
											Phe					/245
	2325					2330		-1-			2335	•••			шуб	
											GCA					7293
Glu	Arg	Gln	Glu	Ile	Gln	Asn	Pro	Asn	Phe	Thr	Ala	Pro	Gly	Gln	Glu	
2340					2345				;	2350				:	2355	
mmm	ama	шош	***	mam.	G3.55			~								
											ACT					7341
FIIC	пец	ser		2360	HIS	ьeu	Tyr			ьeu	Thr	ьeu		_	Ser	
			•	2360				•	2365					2370		
TCA	AGC	AAT	тта	GCA	GTT	тса	GGA	СУТ	CCA	արդար	TAT	CDD	CTT	ጥርጥ	CCT	7389
											Tyr					1309
			2375					2380			-1-		2385	JCI	AIG	
												-	-000			
ACA	AGA	AAT	GAA	AAA	ATG	AGA	CAC	TTG	ATT	ACT	ACA	GGC	AGA	CCA	ACC	7437
Thr	Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly	Arg	Pro	Thr	
	2	2390				2	2395				2	2400				
	~~~															
											CAT					7485
	vai 2405	Pne	vai	Pro			Lys	Thr	Lys		His	Phe	His	Arg	Val	
4	2405				4	2410				•	2415					
GAA	CAG	TGT	GTT	AGG	AAT	АТТ	AAC	TTG	GAG	GAA	AAC	ΔCΩ	م م ص	ΔAG	CAA	7533
											Asn					7333
2420		•			2425					2430		9	0111	-	2435	
											AAT					7581
Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys	Ile	Asn	Asp	
			2	2440				2	2445				2	450		
2 2 00	C 7 C	3 000	~ m	~~~												
											AAT					7629
ASII	GIU		HIS 2455	GIN	Pne	Asn			Asn	Ser	Asn			Ala	Ala	
			.433				4	460				2	465			
GTA	ACT	TTC	ACA	AAG	TGT	GAA	GAA	GAA	ССТ	тта	GAT	ттъ	ΔΤΤ	۵۵۵	ΔСТ	7677
											Asp					7077
		470		•	_		2475				_	2480			501	
											ATT					7725
Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys	Lys	Lys	Gln	
2	485				2	490				2	495					
700	רא א	aca	OTTO	mmm.	GG3	an a	~~ <u>~</u>	999	3 C C	OE C	<b></b>	OF	~~-			
											TAT					7773
2500	O 1 1 1	A	v ca ±		505	GIII	FIO	дту		ьеи 2510	Tyr	ьeu	нта	_		
-500				2					2					2	515	
TCC	ACT	CTG	CCT	CGA	ATC	TCT	CTG	AAA	GCA	GCA	GTA	GGA	GGC	CAA	GTT	7821
											Val					, , , ,
				520					525			4	_	530		
														-		

		GCG Ala					Gln					Gly				7869
	Cys	ATA Ile 2550				Ser					Ser					7917
Thr		GAT Asp			Gly					Trp						7965
		GCT Ala		Gly					Pro					Lys		8013
		GAA Glu	Glu					Leu					Gly			8061
Pro	Lys		Ile 2615	Ser	Arg	Ile	Trp	Val 2620	Tyr	Asn	His	Tyr 2	Arg 2625	Trp	Ile	8109
Ile	Trp	AAA Lys 2630	Leu	Ala	Ala	Met 2	Glu 2635	Cys	Ala	Phe	Pro 2	Lys 2640	Glu	Phe	Ala	8157
Asn		TGC Cys			Pro					Leu						8205
		ACG Thr		Ile					Arg					Lys		8253
		AGG Arg	Asp					Lys					Cys			8301
	_	ATT Ile					Asn					Ser				8349
Thr	Ser	AGT Ser 2710	Ala	Asp	Thr	Gln 2	Lys 2715	Val	Ala	Ile	Ile 2	Glu 2720	Leu	Thr	Asp	8397
Gly		TAT Tyr			Lys					Pro						8445
TTA Leu		AAT														8493

		CTG Leu	Val					Ala					Glu			8541
		CTT Leu					Ser					Arg				8589
	Tyr	ACC Thr 2790				Phe					Arg					8637
Pro		TCA Ser			Phe					Asn						8685
		ATT Ile		Arg					Gln					Thr		8733
		TTA Leu	Tyr					Glu					Lys			8781
		TAT Tyr					Gln					Ala				8829
	Ile	CAG Gln 2870				Glu					Asn					8877
Tyr		CCA Pro			Ala					Gln						8925
		GCA Ala		Leu					Lys					Pro		8973
		GAG Glu	Gly					Glu					Leu			9021
		CAA Gln					Lys					Ile				9069
	Arg	AAG Lys 2950				Ser		-	-	_	Glu	_				9117
Arg		GTC Val			Val					Ile						9165
AAA	GAA	AAA	GAT	TCA	GTT	ATA	CTG	AGT	ATT	TGG	CGT	CCA	TCA	TCA	GAT	9213

Lys 2980	Glu	Lys	Asp		Val 2985	Ile	Leu	Ser		Trp 2990	Arg	Pro	Ser		Asp 2995	
TTA Leu	TAT Tyr	TCT Ser	Leu	TTA Leu 3000	Thr	GAA Glu	GGA Gly	AAG Lys	AGA Arg 3005	TAC Tyr	AGA Arg	ATT Ile	Tyr	CAT His 3010	CTT Leu	9261
GCA Ala	ACT Thr	Ser	AAA Lys 3015	TCT Ser	AAA Lys	AGT Ser	Lys	TCT Ser 3020	GAA Glu	AGA Arg	GCT Ala	Asn	ATA Ile 3025	CAG Gln	TTA Leu	9309
GCA Ala	Ala	ACA Thr 3030	AAA Lys	AAA Lys	ACT Thr	Gln	TAT Tyr 3035	CAA Gln	CAA Gln	CTA Leu	Pro	GTT Val 3040	TCA Ser	GAT Asp	GAA Glu	9357
Ile					Tyr			CGG Arg		Pro						9405
				Asp				TCT Ser	Cys					Leu		9453
GGA Gly	TTT Phe	GTC Val	Val	TCT Ser 3080	GTT Val	GTG Val	AAA Lys	AAA Lys	ACA Thr 3085	GGA Gly	CTT Leu	GCC Ala	Pro	TTC Phe	GTC Val	9501
TAT Tyr	TTG Leu	Ser	GAC Asp 8095	GAA Glu	TGT Cys	TAC Tyr	Asn	TTA Leu 3100	CTG Leu	GCA Ala	ATA Ile	Lys	TTT Phe 105	TGG Trp	ATA Ile	9549
	Leu					Ile		CCT Pro			Leu					9597
Asn					Pro			AAA Lys		Gly						9645
GCT Ala 3140	GGA Gly	GAT Asp	TTT Phe	Ser	GTG Val 3145	TTT Phe	TCT Ser	GCT Ala	Ser	CCA Pro	AAA Lys	GAG Glu	GGC Gly	His	TTT Phe	9693
CAA Gln	GAG Glu	ACA Thr	Phe	AAC Asn 160	AAA Lys	ATG Met	AAA Lys	AAT Asn 3	ACT Thr 165	GTT Val	GAG Glu	AAT Asn	Ile	GAC Asp 170	ATA Ile	9741
CTT Leu	TGC Cys	Asn	GAA Glu 175	GCA Ala	GAA Glu	AAC Asn	Lys	CTT Leu 180	ATG Met	CAT His	ATA Ile	Leu	CAT His 185	GCA Ala	AAT Asn	9789
GAT Asp	Pro					Pro					Thr					9837
ACT Thr	GCT Ala	CAA Gln	ATC Ile	ATT Ile	CCT Pro	GGT Gly	ACA Thr	GGA Gly	AAC Asn	AAG Lys	CTT Leu	CTG Leu	ATG Met	TCT Ser	TCT Ser	9885

CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
  - (A) NAME/KEY: variation
  - (B) LOCATION: 1132
  - (D) OTHER INFORMATION: Xaa = Lys (from codon AAR, R = A or G).

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 10 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 100 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 140 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 165 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 180 185 190 Ser Trp Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 220 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 230 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 250 245 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 260 265 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro 280 285 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu 295 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu 310 315 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala

```
325
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                           360
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
                                            380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                        395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
               405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
            420
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                       475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                        555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                   570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
                               585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                           600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                       615
                                            620
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                    630
                                        635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                645
                                    650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
                                665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                            680
                                                685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695 ~
                                            700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                    710
                                        715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
               725
                                    730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
                                                765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
    770
                        775
```

```
Ile Ser Arq Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                   790
                                      795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                  810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
           820
                              825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                          840
                                              845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                      855
                                          860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                   870
                                      875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
               885
                                  890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
           900
                              905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                          920
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                      935
                                         940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                  950
                                      955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
               965
                                  970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
           980
                              985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                           1000
                                              1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                      1015
                                         1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                  1030
                                      1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
              1045 1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
          1060
                              1065
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                          1080
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                       1095
                                          1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                   1110
                                      1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile
               1125
                                  1130
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
                              1145
           1140
                                                  1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
                          1160
                                             1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                      1175
                                          1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                 1190
                          1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
               1205
                                  1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
           1220
                               1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
```

1235		124	0		1245	
Glu Glu Thr Se	r Ala Glu			Ser Leu 126	Ser Ser	Ser Lys
Cys His Asp Se: 1265	r Val Val 127		Phe Lys	Ile Glu 1275	Asn His	Asn Asp 1280
Lys Thr Val Se	r Glu Lys 1285	Asn Asn	Lys Cys 129		Ile Leu	Gln Asn 1295
Asn Ile Glu Me		Gly Thr	Phe Val	Glu Glu	Ile Thr	
Tyr Lys Arg Ass 1315	n Thr Glu	Asn Glu 132	_	Lys Tyr	Thr Ala 1325	Ala Ser
Arg Asn Ser His	s Asn Leu	Glu Phe 1335	Asp Gly	Ser Asp		Lys Asn
Asp Thr Val Cys	135	0		1355		1360
Gln His Asn Ile	1365	_	137	0	_	1375
Asn Thr Gln Ile	80	_	1385		1390	)
Ala Lys Ala Gli 1395		140	0		1405	
Leu Thr Ala Th	•	1415		142	0	
Asp Thr Phe Pho 1425	143	0		1435		1440
Glu Ser Phe Ass	1445		145	0	_	1455
Leu His Asn Pho		Asn Ser	1465	His Ser	Asp 11e 1470	
		a =				
Asn Lys Met As 1475	o Ile Leu	148	Glu Glu 0	_	Ile Val 1485	Lys His
Asn Lys Met As 1475 Lys Ile Leu Lys 1490	o Ile Leu s Glu Ser	148 Val Pro 1495	Glu Glu 0 Val Gly	Thr Gly	Ile Val 1485 Asn Gln O	Lys His Leu Val
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505	o Ile Leu s Glu Ser y Gln Pro 151	148 Val Pro 1495 Glu Arg 0	Glu Glu O Val Gly	Thr Gly 1500 Lys Ile 1515	Ile Val 1485 Asn Gln O Lys Glu	Lys His Leu Val Pro Thr 1520
Asn Lys Met As 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe	Glu Ser Gln Pro 151 His Thr 1525	148 Val Pro 1495 Glu Arg O Ala Ser	Glu Glu O Val Gly Asp Glu Gly Lys 153	Thr Gly 150 Lys Ile 1515 Lys Val	Ile Val 1485 Asn Gln O Lys Glu Lys Ile	Lys His Leu Val Pro Thr 1520 Ala Lys 1535
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Pho Glu Ser Leu Asy 156	Glu Ser Glu Pro 151 His Thr 1525 Lys Val	148 Val Pro 1495 Glu Arg O Ala Ser	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe	Thr Gly 150 Lys Ile 1515 Lys Val 0 Asp Glu	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1550	Lys His  Leu Val  Pro Thr 1520  Ala Lys 1535  Gln Gly
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 157 Thr Ser Glu Ile 1555	o Ile Leu s Glu Ser y Gln Pro 151 e His Thr 1525 o Lys Val 40 e Thr Ser	Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr	Thr Gly 150 Lys Ile 1515 Lys Val 0 Asp Glu	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1550 Lys Thr	Lys His  Leu Val  Pro Thr 1520  Ala Lys 1535  Gln Gly  Leu Lys
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale	Glu Ser Glu Ser Gln Pro 151 His Thr 1525 Lys Val 40 Thr Ser A Cys Lys	Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr	Thr Gly 150 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala Ala Cys 158	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1550 Lys Thr 1565 Glu Thr	Lys His  Leu Val  Pro Thr 1520  Ala Lys 1535  Gln Gly  Leu Lys  Ile Glu
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585	o Ile Leu s Glu Ser y Gln Pro 151 e His Thr 1525 o Lys Val 40 e Thr Ser a Cys Lys a Pro Lys 159	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr O Glu Leu	Thr Gly 1500 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala 1 Ala Cys 1580 Gln Asn 1595	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1550 Lys Thr 1565 Glu Thr 0 Ser Leu	Lys His  Leu Val  Pro Thr 1520  Ala Lys 1535  Gln Gly  Leu Lys  Ile Glu  Asn Asn 1600
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585 Asp Lys Asn Lei	Glu Ser Glu Ser Gln Pro 151 His Thr 1525 Lys Val Thr Ser Cys Lys Pro Lys 159 Val Ser 1605	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys O Ile Glu	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr Glu Leu Glu Met	Thr Gly 1500 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala 1 Ala Cys 1580 Gln Asn 1595 Val Pro	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1550 Lys Thr 1565 Glu Thr 0 Ser Leu Pro Lys	Lys His  Leu Val  Pro Thr 1520 Ala Lys 1535 Gln Gly Leu Lys Ile Glu Asn Asn 1600 Leu Leu 1615
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585 Asp Lys Asn Lee Ser Asp Asn Lee	Glu Ser Glu Ser Gln Pro 151 His Thr 1525 Lys Val Gran Cys Lys A Pro Lys 159 Val Ser 1605 Cys Arg	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys O Ile Glu Gln Thr	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Gln Glu Leu Glu Met Thr Val 161 Glu Asn 1625	Thr Gly 1500 Lys Ile 1515 Lys Val 0 A Asp Glu Trp Ala 1 Ala Cys 158 CGln Asn 1595 Val Pro 0 Leu Lys	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1556 Lys Thr 1565 Glu Thr 0 Ser Leu Pro Lys Thr Ser 1630	Lys His  Leu Val  Pro Thr 1520 Ala Lys 1535 Gln Gly  Leu Lys  Ile Glu  Asn Asn 1600 Leu Leu 1615 Lys Ser
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585 Asp Lys Asn Lee 166 Ile Phe Leu Lys 1635	o Ile Leu s Glu Ser y Gln Pro 151 e His Thr 1525 o Lys Val 40 e Thr Ser a Cys Lys a Pro Lys 159 u Val Ser 1605 u Cys Arg 20 s Val Lys	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys O Ile Glu Gln Thr Val His	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Gln Glu Leu Glu Met Thr Val 161 Glu Asn 1625 Glu Asn	Thr Gly 150 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala Ala Cys 158 Gln Asn 1595 Val Pro 0 Leu Lys Val Glu	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1556 Lys Thr 1565 Glu Thr 0 Ser Leu Pro Lys Thr Ser 1630 Lys Glu 1645	Lys His  Leu Val  Pro Thr 1520 Ala Lys 1535 Gln Gly  Leu Lys  Ile Glu  Asn Asn 1600 Leu Leu 1615 Lys Ser  Thr Ala
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 155 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585 Asp Lys Asn Lee 166 Ile Phe Leu Lys	o Ile Leu  Go Ile	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys O Ile Glu Gln Thr Val His 164 Tyr Thr 1655	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr Glu Leu Glu Met Thr Val 161 Glu Asr 1625 Glu Asr	Thr Gly 150 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala Ala Cys 158 Coln Asn 1595 Val Pro 10 Leu Lys Val Glu Ser Pro 166	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1556 Lys Thr 1565 Glu Thr 0 Ser Leu Pro Lys Thr Ser 1630 Lys Glu 1645 Tyr Ser 0	Lys His  Leu Val  Pro Thr 1520 Ala Lys 1535 Gln Gly  Leu Lys  Ile Glu  Asn Asn 1600 Leu Leu 1615 Lys Ser  Thr Ala  Val Ile
Asn Lys Met Asy 1475 Lys Ile Leu Lys 1490 Thr Phe Gln Gly 1505 Leu Leu Gly Phe Glu Ser Leu Asy 1555 Thr Ser Glu Ile 1555 Tyr Arg Glu Ale 1570 Ile Thr Ala Ale 1585 Asp Lys Asn Lex Ser Asp Asn Lex 1635 Lys Ser Pro Ale 1650	o Ile Leu  s Glu Ser  y Gln Pro 151 e His Thr 1525 o Lys Val 40 e Thr Ser a Cys Lys 159 u Val Ser 1605 u Cys Arg 20 s Val Lys a Thr Cys a Leu Ala 167	148 Val Pro 1495 Glu Arg O Ala Ser Lys Asn Phe Ser 156 Asp Leu 1575 Cys Lys O Ile Glu Gln Thr Val His Tyr Thr 1655 Phe Tyr O	Glu Glu O Val Gly Asp Glu Gly Lys 153 Leu Phe 1545 His Glr Glu Leu Glu Met Thr Val 161 Glu Asr 1625 Glu Asr 0 Asn Glr	Thr Gly 1500 Lys Ile 1515 Lys Val 0 Asp Glu Trp Ala 1 Ala Cys 1580 Coll Asn 1595 Val Pro 10 1 Leu Lys 1 Val Glu 1 Ser Pro 1666 Cys Ser 1675	Ile Val 1485 Asn Gln 0 Lys Glu Lys Ile Lys Glu 1556 Lys Thr 1565 Glu Thr 0 Ser Leu Pro Lys Thr Ser 1630 Lys Glu 1645 Tyr Ser 0 Arg Lys	Lys His  Leu Val  Pro Thr 1520 Ala Lys 1535 Gln Gly  Leu Lys  Ile Glu  Asn Asn 1600 Leu Leu 1615 Lys Ser  Thr Ala  Val Ile  Thr Ser 1680

```
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
          1700
                1705
                                  1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
     1715
              1720
                                       1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                   1735
                          1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
               1750 1755 1760
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
             1765 1770 1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
         1780 1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
      1795
                       1800
                                        1805
Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn
                   1815
                                     1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                       1835
       1830
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
            1845 1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
         1860 1865 1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
      1875 1880 1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                   1895 1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                1910
                                 1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
                              1930
             1925
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
         1940 1945
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                      1960
                                       1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
                   1975
                                    1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
                1990
                                 1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
             2005
                              2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
         2020
                          2025
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
                       2040
                                        2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                   2055
                                    2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
               2070
                                2075 2080
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
             2085
                             2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
        2100 2105
                                           2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
                       2120
                                       2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                    2135
                                     2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
```

2145	2150	2155	2160
Asp Lys Gln Gln Leu 216	5	Lys Val Ser Leu V 2170	al Glu Asn 2175
Ile His Val Leu Gly 2180	2185	5 2	2190
Glu Ile Gly Lys Thr 2195	2200	2205	
Ile Glu Val Cys Ser 2210	2215	2220	
Thr Glu Ala Val Glu 2225	Ile Ala Lys Ala 2230	Phe Met Glu Asp A 2235	Asp Glu Leu 2240
Thr Asp Ser Lys Leu 224	5	2250	2255
Pro Glu Asn Glu Glu 2260	2265	5 2	270
Arg Gly Glu Pro Leu 2275	Ile Leu Val Gly 2280	Glu Pro Ser Ile I 2285	ys Arg Asn
Leu Leu Asn Glu Phe 2290	2295	2300	_
Lys Ala Ser Lys Ser 2305	2310	2315	2320
Phe Met His His Val 232	5	2330	2335
Thr Thr Lys Glu Arg 2340	2345	5 2	350
Gly Gln Glu Phe Leu 2355	2360	2365	
Glu Lys Ser Ser Ser 2370	2375	2380	
Val Ser Ala Thr Arg 2385	2390	2395	2400
Arg Pro Thr Lys Val 240	5	2410	2415
His Arg Val Glu Gln 2420	2425	2	430
Gln Lys Gln Asn Ile 2435	2440	2445	-
Ile Asn Asp Asn Glu 2450	2455	2460	
Ala Ala Ala Val Thr 2465	2470	2475	2480
Ile Thr Ser Leu Gln 248	5	2490	2495
Lys Lys Gln Arg Gln 2500	2505	2	510
Ala Lys Thr Ser Thr 2515	2520	2525	_
Gly Gln Val Pro Ser 2530	2535	2540	
Val Ser Lys His Cys 2545	2550	2555	2560
Gln Phe His Thr Glu 256!	5	2570	2575
Lys Gly Ile Gln Leu 2580	Ala Asp Glv Glv	Trp Leu Ile Pro S	er Asn Asp
Gly Lys Ala Gly Lys	2585	2	590

```
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
   2610
           2615
                            2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
          2630
                                  2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
             2645
                    2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile
                          2665 2670
    2660
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
     2675 2680 2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
                    2695
                                      2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
                 2710
                                  2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
              2725
                              2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
                          2745
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
      2755
                               2765
              2760
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
   2770 2775
                                     2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
      2790
                                 2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
             2805
                               2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
          2820
                           2825
                                             2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
                       2840
                                         2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arq Leu Glu Ala
          2855
                                     2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                 2870
                                  2875 2880
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
             2885
                              2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
         2900
                          2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
                        2920
                                         2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                    2935
                                     2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
                 2950
                                  2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
             2965
                              2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
                           2985
                                            2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
      2995 3000 3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
   3010
                    3015
                                     3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                3030
                                  3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
                               3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
```

3060 3065 3070 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala 3080 3085 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys 3095 3100 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile 3110 3115 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu 3125 3130 3135 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu 3145 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn 3155 3160 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu 3175 3180 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser 3190 3195 3200 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu 3205 3210 3215 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu 3220 3225 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met 3235 3240 3245 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn 3250 3255 3260 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro 3270 3275 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys 3285 3290 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile 3300 3305 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe 3320 3325 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu 3330 3335 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys 3350 3355 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser 3365 3370 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys 3380 3385 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3400 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile 3410 3415

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT  Met Pro Ile  1	60 120 180 237
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys 5	285
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu 20 25 30 35	333
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu 40 45 50	381
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg 55 60 65	429
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu 70 75 80	477
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp 85 90 95	525
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys 100 115 110 115	573
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser 120 125 130	621
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln 135 140 145	669
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser 150	717
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His 165	765

	GAA Glu								813
	TTA Leu								861
	GAA Glu								909
	AAA Lys 230								957
	TTT Phe								1005
	GCA Ala								1053
	AGC Ser								1101
	GAA Glu								1149
	TTA Leu 310								1197
 	AGC Ser	-							1245
	GAA Glu							_	1293
	GTG Val						_	_	1341
	AAG Lys								1389
	TCT Ser 390								1437

	GGA Gly 405															1485
	CAA Gln															1533
	AAA Lys															1581
	CCA Pro															1629
	GAT Asp															1677
	AAG Lys 485															1725
	ATC Ile															1773
	AAT Asn															1821
	ACT Thr															1869
	AAG Lys															1917
	GCC Ala 565															1965
	TCC Ser															2013
	GAA Glu												_			2061
	CTA Leu															2109
CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157

Pro	Leu	Thr 630	Phe	Ala	Asn	Ala	Asp 635	Ser	Gly	Leu	Leu	His 640	Ser	Ser	Val	
	AGA Arg 645															2205
	AGC Ser															2253
	TCT Ser															2301
	TGT Cys															2349
	CTG Leu															2397
	AAA Lys 725															2445
	GTA Val															2493
	AAA Lys															2541
	CCT Pro															2589
	AAA Lys															2637
	TCT Ser 805															2685
	GTA Val															2733
	GAA Glu															2781
	CAA Gln															2829

855	860	865

										GAC Asp					2877
										GTA Val					2925
										CAT His 910					2973
										ACC Thr					3021
										TCA Ser					3069
										AGT Ser					3117
										GAC Asp					3165
										ATG Met 990					3213
			Pro					Ser		GGA Gly			Phe		3261
GCT Ala		Asn					Leu					Ile			3309
AAA Lys	Met					Ile					Pro				3357
TGT Cys 1					Asn					Asp					3405
AGC Ser 1060				Ser					Ser					Ser	3453
GTA Val			Ser					Ser					Gln		3501

	Asp Phe Asn		AAT TTA ACA CCT Asn Leu Thr Pro 1105	
	Thr Glu Leu		TTA GAA GAA TCA Leu Glu Glu Ser 1120	
			AGC TAC ATA TTG Ser Tyr Ile Leu 1135	
		Asn Gln Met	ACT ATC TTA AAG Thr Ile Leu Lys 1150	
Ser Glu Glu Cys			GTC ATA ATG AAT Val Ile Met Asn	
			TTT GAA GGT ACA Phe Glu Gly Thr 1185	
	Phe Ala Gly		AAT GAC TGT AAC Asn Asp Cys Asn 1200	
			GTG GGG TTT AGG Val Gly Phe Arg 1215	
		Leu Asn Val	TCT ACT GAA GCT Ser Thr Glu Ala 1230	
Lys Ala Val Lys			AAT ATT AGT GAG Asn Ile Ser Glu	
			TCA AGT AAA TGT Ser Ser Lys Cys 1265	
	Met Phe Lys		CAT AAT GAT AAA His Asn Asp Lys 1280	
			TTA CAA AAT AAT Leu Gln Asn Asn 1295	
		Glu Glu Ile	ACT GAA AAT TAC Thr Glu Asn Tyr 1310	

AAT Asn	ACT Thr	'GAA Glu	Asn	GAA Glu 1320	Asp	AAC Asn	AAA Lys	Tyr	ACT Thr 1325	Ala	GCC Ala	AGT Ser	' AGA ' Arg	AAT Asn 1330	TCT Ser	4221
		Leu			GAT Asp		Ser		Ser					Thr	GTT Val	4269
TGT Cys	Ile	CAT His 1350	AAA Lys	GAT Asp	GAA Glu	Thr	GAC Asp 1355	TTG Leu	CTA Leu	TTT Phe	Thr	GAT Asp 1360	Gln	CAC	AAC Asn	4317
Ile	TGT Cys 1365	Leu	AAA Lys	TTA Leu	Ser	GGC Gly 1370	CAG Gln	TTT Phe	ATG Met	Lys	GAG Glu 1375	GGA Gly	AAC Asn	ACT Thr	CAG Gln	4365
				Leu	TCA Ser 1385				Phe					Lys		4413
CAA Gln	GAA Glu	GCA Ala	Cys	CAT His 1400	GGT Gly	AAT Asn	ACT Thr	Ser	AAT Asn 1405	AAA Lys	GAA Glu	CAG Gln	Leu	ACT Thr 1410	GCT Ala	4461
ACT Thr	AAA Lys	Thr	GAG Glu 1415	CAA Gln	AAT Asn	ATA Ile	Lys	GAT Asp 1420	TTT Phe	GAG Glu	ACT Thr	Ser	GAT Asp 1425	ACA Thr	TTT Phe	4509
	Gln				GGG Gly	Lys					Ala					4557
Asn					TTC Phe					Pro						4605
				Ser	GAA Glu 1465				Asp					Lys		4653
			Ser		GAG Glu			Asp					Lys			4701
AAA Lys	GAA Glu	Ser	GTC Val 495	CCA Pro	GTT Val	GGT Gly	Thr	GGA Gly .500	AAT Asn	CAA Gln	CTA Leu	Val	ACC Thr 1505	TTC Phe	CAG Gln	4749
	Gln				GAT Asp	Glu					Pro					4797
Phe					GGG Gly 1					Ile						4845
GAC	AAA	GTG	AAA	AAC	CTT	TTT	GAT	GAA	AAA	GAG	CAA	GGT	ACT	AGT	GAA	4893

Asp 1540	Lys	Val	Lys		Leu 1545	Phe	Asp	Glu	_	Glu 1550	Gln	Gly	Thr		Glu 1555	
		AGT Ser	Phe					Ala					Tyr			4941
_		AAA Lys					Ala					Glu				4989
	Pro	AAG Lys 1590				Met					Asn					5037
Leu		TCT Ser			Thr					Lys						5085
		AGA Arg		Thr					Thr					Phe		5133
		AAA Lys	Val					Glu					Lys			5181
		TGT Cys					Ser					Ile				5229
	Leu	GCT Ala 1670				Ser					Thr					5277
Thr		TTA Leu			Ala					Arg						5325
		CCA Pro		Arg					Asp					Tyr		5373
		AAT Asn	Asn					Ile					Lys			5421
		GAA Glu 1					Tyr					Ser				5469
	Tyr	TCC Ser 1750				Asp					Asp					5517
		AAT Asn														5565

1765 1770 1775

1705	1770	,	1773	
	AAA AAC ACT AGT Lys Asn Thr Ser 1785	Phe Ser Lys		
	GCA TAC CCA CAA Ala Tyr Pro Glr 1800			
Glu Leu Val	ACT AGC TCT TCA Thr Ser Ser Ser 1815			a Ala Ile
	ATA TCT AAT AGT Ile Ser Asn Ser			
	GCC AGT GGT AAA Ala Ser Gly Lys 1850	Ile Val Cys		
	AAA GAC ATA TTT Lys Asp Ile Phe 1865	Thr Asp Ser		
	GAG AAT AAA TCA Glu Asn Lys Ser 1880			
Gly Cys Tyr	GAG GCA TTG GAT Glu Ala Leu Asp 1895			s Asn Ser
	GAT GAA TGT AGO Asp Glu Cys Ser			
	GAA GAA ATT TTA Glu Glu Ile Leu 1930	Gln His Asn		
	TCT AAA ATA TCA Ser Lys Ile Ser 1945	Pro Cys Asp		
	AAA TGT AGT ATA Lys Cys Ser Ile 1960			
Ala Asn Thr	TGT GGG ATT TTT Cys Gly Ile Phe 1975			r Val Gln
	GCT TCA TTA CAA Ala Ser Leu Gln			· -

sp Ser		l Phe S			TTT AAA Phe Lys	6285
			Glu Glu		GCT ATA Ala Ile	6333
	e Ser Gl				AAT GTG Asn Val	6381
er Ala		e Ser T			AAG CAA Lys Gln 2065	6429
				Gly Val	TTA GAG Leu Glu 080	6477
eu Ile		s Ser L			CCT ACG Pro Thr	6525
			rg Val		AGA AAC Arg Asn	6573
	r Glu Me				AAA GAA Lys Glu 2	6621
er Asn		l Glu G			GAA AAT Glu Asn 2145	6669
				Phe Gln	CAA GAC Gln Asp 160	6717
eu Val		s Val S			AAC ATT Asn Ile	6765
			ys Asn		ATG GAA Met Glu	6813
	e Ser As				AAT ATA Asn Ile 2	6861
er Thr			lu Asn '		GAA ACA Glu Thr 2225	6909

	Glu	ATT Ile 2230				Phe					Glu					6957
Lys		CCA Pro			Ala					Phe						7005
		ATG Met		Leu					Ile					Gly		7053
		ATC Ile	Leu					Ser					Leu			7101
		GAC Asp					Asn					Leu				7149
	Ser	ACT Thr 2310				Thr					Arg					7197
His		TCT Ser			Pro					Pro						7245
		CAA Gln		Ile					Phe					Gln		7293
		TCT Ser	Lys					Glu					Glu			7341
		AAT Asn					Gly					Gln				7389
	Arg	AAT Asn 2390				Arg					Thr					7437
Lys		TTT Phe			Pro					Ser						7485
		TGT Cys		Arg					Glu					Lys		7533
		GAT Asp	Gly					Asp					Ile			7581
AAT	GAG	ATT	CAT	CAG	TTT	AAC	AAA	AAC	AAC	TCC	AAT	CAA	GCA	GCA	GCT	7629

Asn	Glu		His 2455	Gln	Phe	Asn	_	Asn 2460	Asn	Ser	Asn		Ala 2465	Ala	Ala	
	Thr					Glu		GAA Glu			Asp					7677
Leu					Asp			GAT Asp		Arg						7725
				Phe				GGC Gly	Ser					Lys		7773
			Pro					AAA Lys					Gly			7821
		Ala					Gln	CTG Leu 2540				Gly		-		7869
	Cys					Ser		AAT Asn			Ser					7917
Thr					Gly			AGT Ser		Trp						7965
				Gly				ATA Ile	Pro					Lys		8013
			Glu					CTG Leu 2					Gly			8061
		Leu					Trp	GTT Val 2620			-	Tyr				8109
	Trp					Met		TGT Cys			Pro					8157
Asn					Pro			GTG Val		Leu						8205
		7 00	C 7 7	א ידיים	CAT	AGA	AGC	AGA	AGA	TCG	GCT	ATA	AAA	AAG	ATA	8253
2660				Ile				Arg	Arg		Ala	Ile	Lys	Lys		

2680 2685 2690

	2680	2685	2690	
	er Leu Ser Ala		ACT TCT AGC AAT Thr Ser Ser Asn 2705	
	la Asp Thr Gln		T ATT GAA CTT ACA E Ile Glu Leu Thr 2720	
			CCC CTC TTA GCT Pro Leu Leu Ala 2735	
			S ATT ATT CTT CAT S Ile Ile Leu His	
			A CCT CTT GAA GCC Pro Leu Glu Ala 2770	Pro
Glu Ser Leu M			T ACT CGG CCT GCT Thr Arg Pro Ala 2785	
	ys Leu Gly Phe		AGA CCT TTT CCT Arg Pro Phe Pro 2800	
			r GTT GGT TGT GTT n Val Gly Cys Val 2815	
			G ATG GAG AAG ACA O Met Glu Lys Thi	
TCT GGA TTA T Ser Gly Leu T	TAC ATA TTT CGC Tyr Ile Phe Arg 2840	AAT GAA AGA GAG Asn Glu Arg Glu 2845	G GAA GAA AAG GAA 1 Glu Glu Lys Glu 2850	ı Ala
Ala Lys Tyr V	eTG GAG GCC CAA /al Glu Ala Gln 355	CAA AAG AGA CTA Gln Lys Arg Leu 2860	A GAA GCC TTA TTO u Glu Ala Leu Pho 2865	C ACT 8829 E Thr
AAA ATT CAG G Lys Ile Gln G 2870	Glu Glu Phe Glu	GAA CAT GAA GAA Glu His Glu Glu 2875	A AAC ACA ACA AA u Asn Thr Thr Ly: 2880	A CCA 8877 S Pro
			A GTT CGT GCT TTO n Val Arg Ala Leo 2895	
GAT GGT GCA C Asp Gly Ala C 2900	GAG CTT TAT GAA Glu Leu Tyr Glu 2905	GCA GTG AAG AA Ala Val Lys Ass 291	T GCA GCA GAC CC. n Ala Ala Asp Pro 0	A GCT 8973 D Ala 2915

	CTT Leu		Gly					Glu					Leu		9021
	AGG Arg	Gln					Lys					Ile			9069
	AGG Arg					Ser					Glu				9117
Arg	GAT Asp 2965				Val					Ile					9165
	GAA Glu			Ser					Ile					Ser	9213
	TAT Tyr		Leu					Lys					Tyr		9261
	ACT Thr	Ser					Lys					Asn			9309
	GCG Ala					Gln					Pro				9357
Ile	TTA Leu 3045				Tyr					Pro					9405
	TTA Leu			Asp					Cys					Leu	9453
	TTT Phe		Val					Lys					Pro		9501
	TTG Leu	Ser					Asn					Lys			9549
	CTT Leu					Ile					Leu				9597
Asn	CTC Leu 3125				Pro					Gly					9645

		GAT Asp		Ser					Ser					His		9693
		ACA Thr	Phe					Asn					Ile			9741
		AAT Asn					Lys					Leu				9789
	Pro	AAG Lys 3190				Pro					Thr					9837
Thr		CAA Gln			Pro					Lys						9885
		TGT Cys		Ile					Pro					Met		9933
		AAG Lys	Ser					Val					Thr			9981
		AAA Lys					Ile					Asn				10029
	Arg	GCC Ala 3270				Leu					Leu					10077
Ser		ATT Ile			Phe					Ala						10125
		AGG Arg		Cys					Glu					Lys		10173
		AAT Asn	Ser					Pro					Asn			10221
		TTG Leu 3					Ile					Leu				10269
	Thr	CAA Gln 350				Ser					Glu					10317
TCT	GTC	AGT	GAA	TCC	ACT	AGG	ACT	GCT	CCC	ACC	AGT	TCA	GAA	GAT	TAT	10365

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3395 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415 10485

#### (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 10 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 60 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 115 120 125 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 140 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 165 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 180 185 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 220

```
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                   230
                                       235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
            260
                               265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                           280
His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                        295
                                            300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                        315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                325
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                       375
                                           380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                   390
                                       395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
               405
                                   410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
        435
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
                                            460
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                   470
                                       475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
               485
                                   490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                               505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                           520
                                               525
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                       535
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                       555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                   570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
                               585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                           600
                                               605
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                       615
                                           620
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                   630
                                       635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
               645
                                   650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
           660
                               665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
```

```
680
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                       695
                                            700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                   710
                                       715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
               725
                                   730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
                                                765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
                                            780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
                               825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                           840
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                       855
                                            860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                   870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
            900
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
                                                925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                   950
                                       955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
               965
                                   970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
           980
                               985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                           1000
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                        1015
                                            1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                    1030
                                       1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
               1045
                                   1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
                               1065
Gln Ser Ser Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                           1080
                                               1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                       1095
                                           1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                   1110
                                       1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
               1125
                                    1130
                                                        1135
```

```
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
           1140
                     1145
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
                         1160
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                    1175
                                      1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                 1190 1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
              1205
                   1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
          1220 1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
                         1240
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                     1255
                                      1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                 1270
                                  1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
                     1290
              1285
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
          1300
                  1305
                                             1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
      1315
               1320
                                         1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                    1335
                                      1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                 1350
                                   1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
              1365
                               1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
          1380
                           1385
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
                        1400
                                          1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
   1410 1415
                                     1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
                1430 1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
                               1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
          1460
                            1465
                                              1470
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
                        1480
                                          1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                    1495
                                      1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                 1510
                                  1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
             1525
                              1530
                                                 1535
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
          1540
                 1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
      1555 1560
                                          1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
                     1575
                                      1580
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
```

1585	1590		1595	1600
Asp Lys Asn Leu	Val Ser Ile 1605	Glu Thr Val		Lys Leu Leu 1615
Ser Asp Asn Leu 1620		Thr Glu Asn 1625		Ser Lys Ser 1630
Ile Phe Leu Lys 1635	Val Lys Val	His Glu Asn 1640	Val Glu Lys G 1645	lu Thr Ala
Lys Ser Pro Ala 1650	165	5	1660	
Glu Asn Ser Ala 1665	1670		1675	1680
Val Ser Gln Thr	1685	169	0	1695
Ile Phe Asp Gly 1700	)	1705	_ 1	710
Asn Tyr Leu Tyr 1715		1720	1725	_
Lys Asn His Leu 1730	173	5	1740	
Met Ser Asn Ser 1745	1750	_	1755	1760
Gly Tyr Leu Ser	1765	177	0	1775
Lys Asn Val Glu 1780	)	1785	1	.790
Asn Val Lys Asp 1795		1800	1805	_
Cys Val Glu Glu 1810	181	5	1820	
Ala Ala Ile Lys 1825	1830		1835	1840
Pro Pro Ala Phe	1845	185	0	1855
Glu Thr Ile Lys 1860	)	1865	1	.870
Val Ile Lys Glu 1875		1880	1885	_
Ile Met Ala Gly 1890	189	5	1900	_
His Asn Ser Leu 1905	1910		1915	1920
Phe Ala Asp Ile	1925	193	0	1935
Ser Gly Leu Glu 1940	)	1945	1	.950
Glu Thr Ser Asp 1955		1960	1965	_
Val Ser Ser Ala 1970	1975	5	1980	
Ser Val Gln Val 1985	1990		1995	2000
Ser Glu Ile Glu	2005	201	0	2015
Lys Ser Asn Glu 2020				
Tlo 1200 mb 10		2025	Lys Gly Phe S	030

```
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
    2050
                     2055
                              2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                 2070
                                    2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
              2085
                               2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
          2100 2105
                                   2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
       2115 2120
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                     2135
                                       2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                  2150
                                    2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
              2165
                                2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
          2180
                            2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
              2200
       2195
                                2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
                     2215 2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                 2230
                                    2235
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
              2245
                                2250
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
           2260
                             2265
                                              2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
       2275
                        2280
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
                    2295
                                       2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
       2310
                                    2315 2320
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
              2325
                                2330
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
          2340
                            2345
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
                         2360
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
                     2375
                                       2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
                  2390
                                   2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
              2405
                                2410
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
          2420
                            2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
                        2440
      2435
                                2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
                     2455
                                       2460
Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu
                  2470
                                    2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
                                2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
```

250	0	2505	2510
	Thr Leu Pro A		Lys Ala Ala Val Gly 2525
Gly Gln Val Pro 2530	Ser Ala Cys S 2535	Ser His Lys Gln	Leu Tyr Thr Tyr Gly 2540
Val Ser Lys His 2545	Cys Ile Lys I 2550	le Asn Ser Lys 2555	Asn Ala Glu Ser Phe 2560
Gln Phe His Thr	Glu Asp Tyr F 2565	Phe Gly Lys Glu 2570	Ser Leu Trp Thr Gly 2575
258	0	2585	Ile Pro Ser Asn Asp 2590
2595	2	2600	Leu Cys Asp Thr Pro 2605
2610	2615		Val Tyr Asn His Tyr 2620
2625	2630	2635	
	2645	2650	Val Leu Leu Gln Leu 2655
266	0	2665	Arg Arg Ser Ala Ile 2670
2675	2	2680	Lys Thr Leu Val Leu 2685
2690	2695		Ile Ser Glu Thr Ser 2700
2705	2710	2715	
	2725	2730	Leu Asp Pro Pro Leu 2735
274	0	2745	Gly Gln Lys Ile Ile 2750
2755	2	2760	Ala Cys Thr Pro Leu 2765
2770	2775	-	Ala Asn Ser Thr Arg
2785	2790	2795	
	2805	2810	Gly Gly Asn Val Gly 2815
282	0	2825	Ile Gln Trp Met Glu 2830
2835	2	2840	Glu Arg Glu Glu Glu 2845
2850	2855		Lys Arg Leu Glu Ala 2860
2865	2870	giu Phe Giu Giu 2875	His Glu Glu Asn Thr 2880
Thr Lys Pro Tyr			
71- T Ol 7	2885	Arg Ala Leu Thr 2890	Arg Gln Gln Val Arg 2895
290	2885 Gly Ala Glu I O	Arg Ala Leu Thr 2890 Leu Tyr Glu Ala 2905	Arg Gln Gln Val Arg 2895 Val Lys Asn Ala Ala 2910
290 Asp Pro Ala Tyr 2915	2885 Gly Ala Glu I O Leu Glu Gly T 2	Arg Ala Leu Thr 2890 Leu Tyr Glu Ala 2905 Tyr Phe Ser Glu	Arg Gln Gln Val Arg 2895 Val Lys Asn Ala Ala 2910 Glu Gln Leu Arg Ala 2925
290 Asp Pro Ala Tyr 2915 Leu Asn Asn His 2930	2885 Gly Ala Glu I O Leu Glu Gly I 2 Arg Gln Met I 2935	Arg Ala Leu Thr 2890 Leu Tyr Glu Ala 2905 Tyr Phe Ser Glu 2920 Leu Asn Asp Lys	Arg Gln Gln Val Arg 2895 Val Lys Asn Ala Ala 2910 Glu Gln Leu Arg Ala

```
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
               2965
                                  2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
           2980
                              2985
                                                 2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
              3000
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                                        3020
                     3015
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                  3030
                                     3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
               3045
                                 3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
                              3065
                                                 3070
           3060
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
       3075
                          3080
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
                                        3100
                      3095
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
                  3110
                                     3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
             3125
                    3130
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
                             3145
           3140
                                                3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
                          3160
       3155
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
                      3175
                                         3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
                  3190
                                     3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
               3205
                                 3210
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
                                                 3230
           3220
                             3225
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
                          3240
                                             3245
       3235
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
                                         3260
                      3255
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
                                     3275
                  3270
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
               3285
                                  3290
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
                             3305
                                                 3310
           3300
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
                          3320
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
           3335
                                         3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
                                     3355
                 3350
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
                                 3370
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
           3380
                             3385
Glu Glu Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
                          3400
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
```

3410 3415

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 229...10482
  - (D) OTHER INFORMATION: BRCA2 (OMI4)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCT(	GCTG( GATT	CGC ( TGT (	CTCG( GACC(	GGTG' GGCG	TC T	FTTG( FTTT	CGGC(	G GTO	GGGT(	CGCC FCCG	GCC	GGGA( AAAA	GAA ( AAG A A AT(	GCGT( AACT( G CC'	TGCGCC GAGGGG GCACCT I ATT D Ile	60 120 180 237
					CCA Pro											285
					GGA Gly 25											333
					CCC Pro											381
					TAC Tyr											429
					CAG Gln											477
					CCG Pro											525
					TTA Leu 105											573
	,				AAA Lys											621

120	125	130	
		CCT GTT GTT CTA Pro Val Val Leu 145	
	g Asp Lys Ser	GTG GTA TGT GGG Val Val Cys Gly 160	
		CAG ACA CCA AAA Gln Thr Pro Lys 175	
		GAT ATG TCT TGG Asp Met Ser Trp	
		ACT GTG CTC ATA Thr Val Leu Ile 210	
		CAT GAT ACT ACT His Asp Thr Thr 225	
	sn His Asp Glu	AGT CTG AAG AAA Ser Leu Lys Lys 240	
		AAC ACA AAT CAA Asn Thr Asn Gln 255	
		GGG AAT TCA TTT Gly Asn Ser Phe	
		ATG CCA AAT GTC Met Pro Asn Val 290	
		TCT GAA GAA GAT Ser Glu Glu Asp 305	
	s Arg Thr Lys	AAT CTA CAA AAA Asn Leu Gln Lys 320	
		GAA GCA AAC GCT Glu Ala Asn Ala 335	
		AAA TAC TCA TTT Lys Tyr Ser Phe	

		AAT Asn								1341
		GAG Glu								1389
		TGT Cys								1437
		GAG Glu								1485
		GAA Glu 425								1533
		ACT Thr								1581
		AAG Lys								1629
		CAT His								1677
		TCT Ser								1725
		ATA Ile 505								1773
		TCA Ser								1821
 	 	 GAA Glu		 		-	_	-		1869
 	 	 TTA Leu	_							1917
		CAG Gln								1965

	TCC Ser															2013
	GAA Glu															2061
	CTA Leu															2109
	CTT Leu															2157
	AGA Arg 645															2205
	AGC Ser															2253
	TCT Ser															2301
	TGT Cys															2349
	CTG Leu															2397
	AAA Lys 725									_						2445
	GTA Val															2493
	AAA Lys															2541
	CCT Pro															2589
_	AAA Lys															2637
GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685

Glu	Ser 805	Asp	Val	Glu	Leu	Thr 810	Lys	Asn	Ile	Pro	Met 815	Glu	Lys	Asn	Gln	
	GTA Val													_		2733
	GAA Glu															2781
	CAA Gln															2829
	TCA Ser															2877
	GAC Asp 885															2925
	CTT Leu															2973
	GTA Val															3021
	ACA Thr															3069
	TAT Tyr															3117
	ATG Met 965															3165
	AAA Lys															3213
	TTA Leu		Pro					Ser					Phe			3261
	TCA Ser	Asn					Leu					Ile				3309
	ATG Met															3357

1030 1035 1040

Cys	Val				AAT Asn											3405
	1045 AAG	CCT	CAG	TCA	ATT	1050 AAT	ACT	GTA	TCT		1055 CAT	TTA	CAG	AGT	AGT	3453
				Ser	Ile 1065				Ser					Ser		
			Ser		TGT Cys			Ser					Gln			3501
		Lys			TTT Phe		Ser					Thr				3549
	Ala				GAA Glu	Leu					Glu					3597
Gln					CAG Gln					Ser						3645
				Val	CCT Pro 1145				Met					Thr		3693
			Cys		GAT Asp			Leu					Asn			3741
		Gly			GAC Asp		Ser					Gly				3789
	Lys	Arg	Lys	Phe	GCT Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	Asn			3837
Ala					ACA Thr					Val						3885
				Gly	ACA Thr 1225				Val					Leu		3933
			Lys		TTT Phe			Ile					Glu			3981
		Glu			CCA Pro		Ser					Lys	-			4029

	Val				TTT Phe	Lys					Asn					4077
Ser					AAA Lys					Leu						4125
				Thr	TTT Phe 1305				Ile					Lys		4173
			Asn		GAT Asp			Tyr					Arg			4221
		Leu			GAT Asp		Ser					Asn				4269
	Ile				GAA Glu	Thr					Thr					4317
Ile					TCT Ser					Lys						4365
_				Leu	TCA Ser 1385				Phe					Lys		4413
Gln	Glu	Ala	Cys 1	His .400	GGT Gly	Asn	Thr	Ser 1	Asn .405	Lys	Glu	Gln	Leu 1	Thr .410	Ala	4461
		Thr			AAT Asn		Lys					Ser				4509
	Gln				GGG Gly	Lys					Ala					4557
Asn					TTC Phe					Pro						4605
				Ser	GAA Glu 1465				Asp					Lys		4653
			Ser		GAG Glu			Asp					Lys			4701

AAA Lys	A GAA S Glu	Ser	GTC Val 1495	CCA Pro	GTT Val	GGT Gly	Thr	GGA Gly 1500	AAT Asn	CAA Gln	CTA Leu	Val	ACC Thr 1505	TTC Phe	CAG Gln	4749
GGA Gly	CAA Gln	CCC Pro 1510	GAA Glu	CGT Arg	GAT Asp	Glu	AAG Lys 1515	ATC Ile	AAA Lys	GAA Glu	CCT Pro	ACT Thr 1520	CTG Leu	TTG Leu	GGT Gly	4797
TTT Phe	CAT His	Thr	GCT Ala	AGC Ser	Gly	AAA Lys 1530	AAA Lys	GTT Val	AAA Lys	Ile	GCA Ala 1535	AAG Lys	GAA Glu	TCT Ser	TTG Leu	4845
GAC Asp 1540	Lys	GTG Val	AAA Lys	Asn	CTT Leu 1545	TTT Phe	GAT Asp	GAA Glu	Lys	GAG Glu 1550	CAA Gln	GGT Gly	ACT Thr	Ser	GAA Glu 1555	4893
ATC Ile	ACC Thr	AGT Ser	Phe	AGC Ser 1560	CAT His	CAA Gln	TGG Trp	Ala	AAG Lys 1565	ACC Thr	CTA Leu	AAG Lys	Tyr	AGA Arg 1570	GAG Glu	4941
GCC Ala	TGT Cys	Lys	GAC Asp 1575	CTT Leu	GAA Glu	TTA Leu	Ala	TGT Cys 1580	GAG Glu	ACC Thr	ATT Ile	Glu	ATC Ile 1585	ACA Thr	GCT Ala	4989
GCC Ala	Pro	AAG Lys 1590	TGT Cys	AAA Lys	GAA Glu	Met	CAG Gln 595	AAT Asn	TCT Ser	CTC Leu	AAT Asn	AAT Asn L600	GAT Asp	AAA Lys	AAC Asn	5037
Leu	GTT Val 1605	TCT Ser	ATT Ile	GAG Glu	Thr	GTG Val 1610	GTG Val	CCA Pro	CCT Pro	Lys	CTC Leu 1615	TTA Leu	AGT Ser	GAT Asp	AAT Asn	5085
TTA Leu 1620	TGT Cys	AGA Arg	CAA Gln	Thr	GAA Glu .625	AAT Asn	CTC Leu	AAA Lys	Thr	TCA Ser 1630	AAA Lys	AGT Ser	ATC Ile	Phe	TTG Leu .635	5133
AAA Lys	GTT Val	AAA Lys	Val	CAT His 640	GAA Glu	AAT Asn	GTA Val	Glu	AAA Lys .645	GAA Glu	ACA Thr	GCA Ala	Lys	AGT Ser .650	CCT Pro	5181
		Cys					Ser				GTC Val	Ile				5229
	Leu					Ser					ACT Thr 1					5277
Thr					Ala					Arg	GAA Glu .695					5325
				Arg					Asp		GTA Val			Tyr		5373
TAT	GAA	AAT	AAT	TCA	AAC	AGT	ACT	ATA	GCT	GAA	AAT	GAC	AAA	AAT	CAT	5421

Tyr	Glu	Asn	Asn 1	Ser L720	Asn	Ser	Thr		Ala 1725	Glu	Asn	Asp	-	Asn 1730	His	
		Glu	AAA Lys 1735				Tyr					Ser	-		_	5469
	Tyr		TAC Tyr			Asp					Asp					5517
Ser			AAA Lys		Asp					Pro						5565
			AAA Lys	Asn					Lys					Val		5613
			GCA Ala					Val					Cys			5661
		Val	ACT Thr 1815				Pro					Asn				5709
	Leu		ATA Ile			Ser					Val					5757
Phe			GCC Ala		Gly					Val					ATT Ile	5805
Phe AAA	Arg 1845 AAA	Ile GTG		Ser GAC Asp	Gly ATA	Lys 1850 TTT	Ile ACA	Val GAC	Cys AGT Ser	Val TTC	Ser 1855 AGT	His AAA	Glu GTA	Thr ATT Ile	Ile AAG	5805 5853
Phe AAA Lys 1860 GAA	Arg 1845 AAA Lys AAC	Ile GTG Val	Ala AAA Lys GAG Glu	GAC Asp	Gly ATA Ile 1865	Lys 1850 TTT Phe	Ile ACA Thr	Val GAC Asp	Cys AGT Ser TGC	TTC Phe 1870	Ser L855 AGT Ser	His AAA Lys AAA	Glu GTA Val ATT Ile	Thr ATT Ile	AAG Lys 1875 GCA	
Phe AAA Lys 1860 GAA Glu GGT	Arg 1845 AAA Lys AAC Asn	GTG Val AAC Asn TAC	Ala AAA Lys GAG Glu	GAC Asp AAT Asn L880	ATA Ile 1865 AAA Lys	Lys 1850 TTT Phe TCA Ser	ACA Thr AAA Lys GAT Asp	Val GAC Asp ATT Ile	AGT Ser TGC Cys	Val TTC Phe 1870 CAA Gln	Ser 1855 AGT Ser ACG Thr	AAA Lys AAA Lys CTT Leu	Glu GTA Val ATT Ile CAT	Thr  ATT Ile ATG Met L890 AAC	AAG Lys 1875 GCA Ala	5853
Phe AAA Lys 1860 GAA Glu GGT Gly CTA	Arg 1845 AAA Lys AAC Asn TGT Cys	GTG Val AAC Asn TAC Tyr	Ala AAA Lys GAG Glu GAG Glu	GAC Asp AAT Asn 1880 GCA Ala	ATA Ile 1865 AAA Lys TTG Leu TGT	Lys 1850 TTT Phe TCA Ser GAT Asp	ACA Thr AAA Lys GAT Asp	GAC Asp  ATT Ile  TCA Ser 1900  CAT	Cys AGT Ser TGC Cys 1885 GAG Glu TCA	TTC Phe 870 CAA Gln GAT Asp	Ser 1855 AGT Ser ACG Thr ATT Ile	AAA Lys AAA Lys CTT Leu	Glu GTA Val ATT Ile CAT His	ATT Ile ATG Met 1890 AAC ASn	AAG Lys 1875 GCA Ala TCT Ser	5853 5901
Phe AAA Lys 1860 GAA Glu GGT Gly CTA Leu ATT Ile	Arg 1845 AAA Lys AAC Asn TGT Cys GAT Asp	GTG Val AAC Asn TAC Tyr AAT Asn 1910	AAA Lys GAG Glu GAG Glu 1895	GAC Asp AAT Asn L880 GCA Ala GAA Glu	ATA Ile 1865 AAA Lys TTG Leu TGT Cys ATT Ile	Lys 1850 TTT Phe TCA Ser GAT Asp	ACA Thr AAA Lys GAT Asp ACG Thr 1915	GAC Asp  ATT Ile  TCA Ser 1900  CAT His	AGT Ser TGC Cys 1885 GAG Glu TCA Ser	TTC Phe 1870 CAA Gln GAT Asp CAT His	Ser 1855 AGT Ser ACG Thr ATT Ile AAG Lys	AAA Lys AAA Lys CTT Leu GTT Val	Glu GTA Val ATT Ile CAT His L905 TTT Phe	ATT Ile ATG Met 1890 AAC Asn GCT Ala	AAG Lys 1875 GCA Ala TCT Ser GAC Asp	5853 5901 5949

1940			;	1945				:	1950				:	1955	
	ATA TG						Lys					Val			6141
	AAT AC Asn Th					Ser					Lys				6189
	TCA GA Ser As	p Ala			Gln	_				Val					6237
Glu	GAT AG Asp Se 2005			Gln					Val						6285
	CAT TC His Se		Gln					Glu					Arg		6333
	GAA CA Glu Hi	s Leu					Gly					Val			6381
	TCT GC Ser Al					Ser					Lys				6429
	TTA GA Leu Gl 207	u Ser			His					Val					6477
Asp	TTA AT Leu Il 2085			Glu					Tyr						6525
	AAT GT Asn Va		Lys					Val					Pro		6573
	TGT GT Cys Va	l Asn					Lys					Glu			6621
	TCA AA Ser As					Glu					Glu				6669
	ATT AA Ile Ly 215	s Val			Tyr					Gln				_	6717
Gln	TTG GT Leu Va 2165			Thr					Val						6765

				Gln	GCT Ala 2185				Asn					Ile	6813
			Thr		TCT Ser			Pro					Ile		6861
		Thr			AAA Lys		Ser					Glu			6909
	Glu				GCT Ala	Phe					Glu				6957
Lys					GCC Ala					Phe					7005
				Leu	TCA Ser 2265				Ile					Gly	7053
			Leu		GGA Gly			Ser					Leu		7101
		Asp			ATA Ile		Asn					Leu			7149
	Ser				GGC Gly	Thr					Arg				7197
His					CCG Pro					Pro					7245
				Ile	CAG Gln 2345				Phe					${\tt Gln}$	7293
			Lys		CAT His			Glu					Glu		7341
		Asn			GTT Val		Gly					Gln			7389
_	Arg				ATG Met	Arg					Thr				7437

Lys					Pro					Ser	CAT His 2415					7485
				Arg					Glu		AAC Asn			Lys		7533
			Gly					Asp			AAT Asn		Ile			7581
		Ile					Lys				AAT Asn	Gln				7629
	Thr					Glu					GAT Asp					7677
Leu					Asp					Arg	ATT Ile 2495					7725
				Phe					Ser		TAT Tyr			Lys		7773
			Pro					Lys			GTA Val		Gly			7821
		Ala					Gln				TAT Tyr	Gly				7869
	Cys					Ser					TCT Ser					7917
Thr					Gly					${\tt Trp}$	ACT Thr 2575					7965
				Gly					Pro		AAT Asn			Lys		8013
			Glu					Leu			ACT Thr		Gly			8061
		Leu					Trp				CAC His	Tyr				8109
ATA	TGG	AAA	CTG	GCA	GCT	ATG	GAA	TGT	GCC	TTT	CCT	AAG	GAA	TTT	GCT	8157

Ile	Trp	Lys 2630	Leu	Ala	Ala		Glu 635	Cys	Ala	Phe		Lys 640	Glu	Phe	Ala	
Asn	AGA Arg 2645				Pro					Leu						8205
	GAT Asp			Ile					Arg					Lys		8253
	GAA Glu		Asp					Lys					Cys			8301
	ATA Ile	Ile					Asn					Ser				8349
	AGT Ser					Gln					Ile					8397
	TGG Trp 2725				Lys					Pro						8445
	AAG Lys			Arg					Gln					His		8493
	GAA Glu		Val					Ala					Glu			8541
	TCT Ser	Leu					Ser					Arg				8589
	TAT	ACC	אאא	~~~												
	-	Thr 2790				Phe					Arg					8637
	-	2790 TCA	Lys TCG	Leu	Gly TTC Phe	Phe Z AGT	Phe 2795 GAT	Pro GGA	Asp GGA	Pro AAT Asn	Arg 2 GTT	Pro 2800 GGT	Phe TGT	Pro GTT	Leu	8637 8685
Pro	TTA Leu 2805 ATT Ile	TCA Ser	TCG Ser	CTT Leu AGA Arg	Gly TTC Phe	Phe AGT Ser 2810	Phe 2795 GAT Asp	Pro GGA Gly ATA	GGA Gly CAG Gln	Pro AAT Asn TGG	Arg GTT Val 2815 ATG	Pro 2800 GGT Gly GAG	TGT Cys	GTT Val ACA Thr	GAT Asp	
Pro GTA Val 2820	TTA Leu 2805 ATT Ile	TCA Ser ATT Ile	TCG Ser CAA Gln TAC	CTT Leu AGA Arg	TTC Phe GCA Ala 2825	Phe AGT Ser 2810 TAC Tyr	Phe 2795 GAT Asp CCT Pro	GGA Gly ATA Ile GAA Glu	GGA Gly CAG Gln	AAT Asn TGG Trp 2830	GTT Val 2815 ATG Met	Pro 2800 GGT Gly GAG Glu	TGT Cys AAG Lys	GTT Val ACA Thr	GAT Asp  TCA Ser 2835 GCA	8685

2855	2860	2865

	Ile	CAG Gln 2870				Glu					Asn					8877
Tyr		CCA Pro			Ala					Gln						8925
		GCA Ala		Leu					Lys					Pro		8973
		GAG Glu	Gly					Glu					Leu			9021
		CAA Gln					Lys					Ile				9069
	Arg	AAG Lys 2950				Ser					Glu				_	9117
Arg		GTC Val			Val					Ile						9165
		AAA Lys		Ser					Ile					Ser		9213
		TCT Ser	Leu					Lys					Tyr			9261
		TCA Ser					Lys					Asn				9309
	Ala	ACA Thr 3030				Gln					Pro					9357
Ile		TTT Phe			Tyr					Pro						9405
		GAT Asp		Asp					Cys					Leu		9453
		GTC Val	Val					Lys					Pro			9501

			A ATA AAG TTT TGG ATA a Ile Lys Phe Trp Ile 3105	
	Asp Ile Ile		G TTA ATT GCT GCA AGC Leu Ile Ala Ala Ser 3120	
			C CTT CTT ACT TTA TTT y Leu Leu Thr Leu Phe 3135	
			A AAA GAG GGC CAC TTT D Lys Glu Gly His Phe 3155	
Gln Glu Thr Phe			F GAG AAT ATT GAC ATA l Glu Asn Ile Asp Ile 3170	
			F ATA CTG CAT GCA AAT S Ile Leu His Ala Asn 3185	
	Ser Thr Pro		F ACT TCA GGG CCG TAC S Thr Ser Gly Pro Tyr 3200	
			G CTT CTG ATG TCT TCT S Leu Leu Met Ser Ser 3215	
			A TCA CTT TGT ATG GCC 1 Ser Leu Cys Met Ala 3235	
Lys Arg Lys Ser			C CAG ATG ACT TCA AAG a Gln Met Thr Ser Lys 3250	
			A AAG AAC TGC AAA AAG n Lys Asn Cys Lys Lys 3265	
	GAT TTC TTG	AGT AGA CTG CCT	T TTA CCT CCA CCT GTT	10077
3270	_	Ser Arg Leu Pro 275	o Leu Pro Pro Pro Val 3280	
3270 AGT CCC ATT TGT	ACA TTT GTT	275 TCT CCG GCT GCA		

			Ser		CAG Gln			Pro					Asn			10221
		Leu	_		AAT Asn		Ile					Leu			ATA Ile	10269
	Thr				TTG Leu	Ser					Glu					10317
Ser					ACT Thr					Thr						10365
				Arg	CGT Arg 3385				Ser					${\tt Gln}$		10413
			Ala		ACG Thr			Cys					Gln		ACA Thr	10461
		Thr			TAT Tyr		TAA									10485

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

 Met
 Pro
 Ile
 Gly
 Ser
 Lys
 Glu
 Arg
 Pro
 Thr
 Phe
 Phe
 Glu
 Ile
 Phe
 Lys
 Lys
 Is
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 15
 10
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20
 20</th

```
115
                            120
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
                        135
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
                   150
                                        155
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
                165
                                    170
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
           180
                                185
Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                            200
                                                205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                        215
                                            220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                    230
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                245
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
                               265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                            280
Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                        295
                                            300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                        315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                325
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
                                                365
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                       375
                                            380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                   390
                                       395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
               405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
           420
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                        475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
                                                525
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
                                            540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                       555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                    570
```

```
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
                                585
            580
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                            600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                        615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                                       635
                    630
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                                   650
                645
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
                                665
            660
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                            680
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                                            700
                        695
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                                       715
                   710
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
                725
                                   730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
            740
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                                                765
                            760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                                            780
                        775
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
                805
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
                                825
            820
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
                                                845
        835
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
                                            860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                                    890
                885
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
                                905
            900
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                                        955
                    950
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
                                    970
                965
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
                                985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                            1000
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                                             1020
                         1015
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
```

1025	1030			1035		1040
Ser Leu Ala Cys	1045		1050			1055
Lys Lys Leu Ser 1060	1	1	1065		1070	)
Gln Ser Ser Val 1075		1080			1085	
Gln Met Leu Phe 1090		1095		1100		
Pro Ser Gln Lys 1105	1110			1115		1120
Ser Gly Ser Gln	1125		1130	)		1135
Leu Gln Lys Ser 1140	)	1	L145		1150	)
Lys Thr Thr Ser 1155		1160			1165	
Asn Ala Pro Ser 1170		1175		1180		
Thr Val Glu Ile 1185	1190			1195		1200
Asn Lys Ser Ala	1205		1210	)		1215
Arg Gly Phe Tyr 1220	)	-	1225		1230	0
Ala Leu Gln Lys 1235		1240			1245	
Glu Glu Thr Ser 1250		1255		1260	1	
Cys His Asp Ser 1265	1270	1		1275		1280
Lys Thr Val Ser	1285		1290	כ		1295
Asn Ile Glu Met 1300	)		1305		131	0
Tyr Lys Arg Asn 1315		1320			1325	
Arg Asn Ser His	Asn Leu	Glu Phe	Asp Glv	Ser Aen		
1330		1335		1340	)	
Asp Thr Val Cys 1345	1350	1335 Lys Asp ( )	Glu Thr	1340 Asp Leu 1355	) Leu Phe	Thr Asp 1360
Asp Thr Val Cys 1345 Gln His Asn Ile	1350 Cys Leu 1365	1335 Lys Asp ( ) Lys Leu (	Glu Thr Ser Gly 137	1340 Asp Leu 1355 Gln Phe	Leu Phe Met Lys	Thr Asp 1360 Glu Gly 1375
Asp Thr Val Cys 1345 Gln His Asn Ile Asn Thr Gln Ile 138	1350 Cys Leu 1365 Lys Glu 0	Lys Asp (  Lys Leu (  Asp Leu (	Glu Thr Ser Gly 137 Ser Asp 1385	1340 Asp Leu 1355 Gln Phe O Leu Thr	Leu Phe Met Lys Phe Leu 139	Thr Asp 1360 Glu Gly 1375 Glu Val 0
Asp Thr Val Cys 1345 Gln His Asn Ile Asn Thr Gln Ile 138 Ala Lys Ala Gln 1395	1350 Cys Leu 1365 Lys Glu O Glu Ala	Lys Asp ( Lys Leu : Asp Leu : Cys His ( 1400	Glu Thr Ser Gly 137 Ser Asp 1385 Gly Asn	Asp Leu 1355 Gln Phe 0 Leu Thr	Leu Phe Met Lys Phe Leu 139 Asn Lys 1405	Thr Asp 1360 Glu Gly 1375 Glu Val O Glu Gln
Asp Thr Val Cys 1345 Gln His Asn Ile Asn Thr Gln Ile 138 Ala Lys Ala Gln 1395 Leu Thr Ala Thr 1410	1350 Cys Leu 1365 Lys Glu O Glu Ala	Lys Asp C Lys Leu : Asp Leu : Cys His : 1400 Glu Gln : 1415	Glu Thr Ser Gly 1376 Ser Asp 1385 Gly Asn Asn Ile	Asp Leu 1355 Gln Phe 0 Leu Thr Thr Ser Lys Asp	Deu Phe Met Lys Phe Leu 139 Asn Lys 1405 Phe Glu	Thr Asp 1360 Glu Gly 1375 Glu Val O Glu Gln Thr Ser
Asp Thr Val Cys 1345 Gln His Asn Ile Asn Thr Gln Ile 1380 Ala Lys Ala Gln 1395 Leu Thr Ala Thr 1410 Asp Thr Phe Phe 1425	1350 Cys Leu 1365 Lys Glu 0 Glu Ala Lys Thr Gln Thr 1430	Lys Asp ( Lys Leu ( Asp Leu ( 1400) Glu Gln ( 1415) Ala Ser	Glu Thr Ser Gly 1370 Ser Asp 1385 Gly Asn Asn Ile Gly Lys	Asp Leu 1355 Gln Phe Leu Thr Thr Ser Lys Asp 1420 Asn Ile 1435	Deu Phe Met Lys Phe Leu 139 Asn Lys 1405 Phe Glu Ser Val	Thr Asp 1360 Glu Gly 1375 Glu Val O Glu Gln Thr Ser Ala Lys 1440
Asp Thr Val Cys 1345 Gln His Asn Ile  Asn Thr Gln Ile 138 Ala Lys Ala Gln 1395 Leu Thr Ala Thr 1410 Asp Thr Phe Phe 1425 Glu Ser Phe Asn	1350 Cys Leu 1365 Lys Glu 0 Glu Ala Lys Thr 1430 Lys Ile 1445	Lys Asp ( Lys Leu ( Asp Leu ( 1400 Glu Gln ( 1415 Ala Ser ( ) Val Asn	Glu Thr Ser Gly 1370 Ser Asp 1385 Gly Asn Asn Ile Gly Lys Phe Phe 145	Asp Leu 1355 Gln Phe 0 Leu Thr Thr Ser Lys Asp 1420 Asn Ile 1435 Asp Gln 0	Leu Phe Met Lys Phe Leu 139 Asn Lys 1405 Phe Glu Ser Val	Thr Asp 1360 Glu Gly 1375 Glu Val O Glu Gln Thr Ser Ala Lys 1440 Glu Glu 1455
Asp Thr Val Cys 1345 Gln His Asn Ile Asn Thr Gln Ile 1380 Ala Lys Ala Gln 1395 Leu Thr Ala Thr 1410 Asp Thr Phe Phe 1425	1350 Cys Leu 1365 Lys Glu 0 Glu Ala Lys Thr 1430 Lys Ile 1445 Ser Leu 0	Lys Asp ( Lys Leu ( Asp Leu ( Asp Leu ( 1400 Glu Gln ( 1415 Ala Ser ( ) Val Asn Asn Ser	Glu Thr Ser Gly 1376 Ser Asp 1385 Gly Asn Asn Ile Gly Lys Phe Phe 145 Glu Leu 1465	Asp Leu 1355 Gln Phe 0 Leu Thr Thr Ser Lys Asp 1420 Asn Ile 1435 Asp Gln 0 His Ser	Leu Phe Met Lys Phe Leu 139 Asn Lys 1405 Phe Glu Ser Val Lys Pro Asp Ile 147	Thr Asp 1360 Glu Gly 1375 Glu Val 0 Glu Gln Thr Ser Ala Lys 1440 Glu Glu 1455 Arg Lys

```
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                      1495
                                        1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                  1510
                                    1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
              1525
                     1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
         1540 1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
      1555 1560
                                           1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
                     1575
                                       1580
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
                  1590
                                    1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
              1605
                                 1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
                            1625
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
      1635 1640
                                           1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
                                       1660
          1655
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
                 1670
                                    1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
              1685
                                 1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
          1700
                             1705
                                               1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
       1715
                        1720
                                           1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                     1735
                                       1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
                 1750
                                    1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
              1765 1770
                                                  1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
          1780
                            1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
                         1800
                                            1805
Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn
                      1815
                                        1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                  1830
                                    1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
              1845
                                1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
          1860
                            1865
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
                         1880
                                           1885
       1875
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                     1895
                           1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                  1910
                                    1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
              1925
                                 1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
```

	)	194	5		1950	
Glu Thr Ser Asp 1955	Ile Cys Ly			Lys Leu 1969	His Lys	Ser
Val Ser Ser Ala 1970	Asn Thr Cy	_	Phe Ser	Thr Ala 1980	Ser Gly	Lys
Ser Val Gln Val 1985	Ser Asp Al. 1990	a Ser Leu	Gln Asn 1995		Gln Val	Phe 2000
Ser Glu Ile Glu	Asp Ser Th 2005	r Lys Gln	Val Phe 2010	Ser Lys	Val Leu 2015	
Lys Ser Asn Glu 2020		p Gln Leu 202		Glu Glu	Asn Thr 2030	Ala
Ile Arg Thr Pro 2035		2040	_	2045	5	
Val Val Asn Ser 2050	20	55		2060	_	_
Gln Val Ser Ile 2065	2070		2075	;	_	2080
Glu Glu Phe Asp	2085		2090		2095	5
Thr Ser Arg Gln 2100	)	210	5	_	2110	_
Asn Pro Glu His 2115	_	2120		2125	5	_
Glu Phe Lys Leu 2130	21	35		2140		
Asn Asn His Ser 2145	2150		2155	;		2160
Asp Lys Gln Gln	2165	u Gly Thr	Lys Val 2170	Ser Leu	Val Glu 2175	
					<b>-</b> -	
Ile His Val Leu 2180	)	218	5	_	2190	
2180 Glu Ile Gly Lys 2195	) Thr Glu Th	218 r Phe Ser 2200	5 Asp Val	Pro Val	2190 Lys Thr	Asn
2180 Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210	Thr Glu Th Ser Thr Ty 22	218 r Phe Ser 2200 r Ser Lys 15	5 Asp Val Asp Ser	Pro Val 2205 Glu Asn 2220	2190 Lys Thr Tyr Phe	Asn Glu
Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225	Thr Glu Th Ser Thr Ty 22 Glu Ile Al 2230	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala	Asp Val Asp Ser Phe Met 2235	Pro Val 2205 Glu Asn 2220 Glu Asp	2190 Lys Thr 5 Tyr Phe Asp Glu	Asn Glu Leu 2240
Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys	Thr Glu Th Ser Thr Ty 22 Glu Ile Al 2230 Leu Pro Se 2245	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala	Asp Val Asp Ser  Phe Met 2235 Thr His 2250	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255	Asn Glu Leu 2240 Cys
Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys Pro Glu Asn Glu 2260	Thr Glu Th  Ser Thr Ty  22 Glu Ile Al. 2230  Leu Pro Se 2245 Glu Met Va	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270	Asn Glu Leu 2240 Cys Arg
Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys Pro Glu Asn Glu 2260 Arg Gly Glu Pro 2275	Thr Glu Th  Ser Thr Ty 22 Glu Ile Al 2230 Leu Pro Se 2245 Glu Met Va Leu Ile Le	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser 5 Glu Pro	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285	Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg	Asn Glu Leu 2240 Cys Arg Asn
2180 Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys  Pro Glu Asn Glu 2260 Arg Gly Glu Pro 2275 Leu Leu Asn Glu 2290	Thr Glu Th  Ser Thr Ty 22 Glu Ile Al 2230  Leu Pro Se 2245 Glu Met Va  Leu Ile Le  Phe Asp Ar 22	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Ser	Asn Glu Leu 2240 Cys Arg Asn Leu
Glu Ile Gly Lys 2195  Ile Glu Val Cys 2210  Thr Glu Ala Val 2225  Thr Asp Ser Lys  Pro Glu Asn Glu 2260  Arg Gly Glu Pro 2275  Leu Leu Asn Glu 2290  Lys Ala Ser Lys 2305	Thr Glu Th  Ser Thr Ty 22 Glu Ile Al. 2230 Leu Pro Se 2245 Glu Met Va Leu Ile Le  Phe Asp Are 22 Ser Thr Pre 2310	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95 o Asp Gly	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn Thr Ile 2315	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300 Lys Asp	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Ser Arg Arg	Asn Glu Leu 2240 Cys Arg Asn Leu Leu 2320
Glu Ile Gly Lys 2195  Ile Glu Val Cys 2210  Thr Glu Ala Val 2225  Thr Asp Ser Lys  Pro Glu Asn Glu 2260  Arg Gly Glu Pro 2275  Leu Leu Asn Glu 2290  Lys Ala Ser Lys  2305  Phe Met His His	Thr Glu Th  Ser Thr Ty 22 Glu Ile Al. 2230 Leu Pro Se. 2245 Glu Met Va Leu Ile Le  Phe Asp Are 22 Ser Thr Pro 2310 Val Ser Le 2325	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95 o Asp Gly u Glu Pro	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn Thr Ile 2315 Ile Thr 2330	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300 Lys Asp Cys Val	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Ser Arg Arg Pro Phe 2335	Asn Glu Leu 2240 Cys Arg Asn Leu Leu 2320 Arg
Glu Ile Gly Lys 2195  Ile Glu Val Cys 2210  Thr Glu Ala Val 2225  Thr Asp Ser Lys  Pro Glu Asn Glu 2260  Arg Gly Glu Pro 2275  Leu Leu Asn Glu 2290  Lys Ala Ser Lys 2305  Phe Met His His  Thr Thr Lys Glu 2340	Thr Glu Th  Ser Thr Ty  22 Glu Ile Al. 2230  Leu Pro Se. 2245 Glu Met Va  Leu Ile Le  Phe Asp Ar. 22  Ser Thr Pr. 2310  Val Ser Le 2325  Arg Gln Gl	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95 o Asp Gly u Glu Pro u Ile Gln 234	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn Thr Ile 2315 Ile Thr 2330 Asn Pro 5	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300 Lys Asp Cys Val Asn Phe	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Ser Arg Arg Pro Phe 2335 Thr Ala 2350	Asn Glu Leu 2240 Cys Arg Asn Leu 2320 Arg Pro
2180 Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys  Pro Glu Asn Glu 2260 Arg Gly Glu Pro 2275 Leu Leu Asn Glu 2290 Lys Ala Ser Lys 2305 Phe Met His His Thr Thr Lys Glu 2340 Gly Gln Glu Phe 2355	Thr Glu Th  Ser Thr Ty  22 Glu Ile Al.  2230  Leu Pro Se  2245 Glu Met Va  Leu Ile Le  Phe Asp Ar  22  Ser Thr Pr  2310  Val Ser Le  2325  Arg Gln Gl  Leu Ser Ly	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95 o Asp Gly u Glu Pro u Ile Gln 234 s Ser His 2360	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn Thr Ile 2315 Ile Thr 2330 Asn Pro 5 Leu Tyr	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300 Lys Asp Cys Val Asn Phe Glu His 2365	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Arg Lys Arg Pro Phe 2335 Thr Ala 2350 Leu Thr	Asn Glu Leu 2240 Cys Arg Asn Leu 2320 Arg Pro
2180 Glu Ile Gly Lys 2195 Ile Glu Val Cys 2210 Thr Glu Ala Val 2225 Thr Asp Ser Lys  Pro Glu Asn Glu 2260 Arg Gly Glu Pro 2275 Leu Leu Asn Glu 2290 Lys Ala Ser Lys 2305 Phe Met His His Thr Thr Lys Glu 2340 Gly Gln Glu Phe	Thr Glu Th  Ser Thr Ty 22 Glu Ile Al 2230  Leu Pro Se 2245 Glu Met Va  Leu Ile Le  Phe Asp Ar 22 Ser Thr Pr 2310  Val Ser Le 2325  Arg Gln Gl  Leu Ser Ly  Ser Asn Le 23	218 r Phe Ser 2200 r Ser Lys 15 a Lys Ala r His Ala l Leu Ser 226 u Val Gly 2280 g Ile Ile 95 o Asp Gly u Glu Pro u Ile Gln 234 s Ser His 2360 u Ala Val 75	Asp Val Asp Ser Phe Met 2235 Thr His 2250 Asn Ser Glu Pro Glu Asn Thr Ile 2315 Ile Thr 2330 Asn Pro 5 Leu Tyr Ser Gly	Pro Val 2205 Glu Asn 2220 Glu Asp Ser Leu Arg Ile Ser Ile 2285 Gln Glu 2300 Lys Asp Cys Val Asn Phe Glu His 2365 His Pro 2380	2190 Lys Thr Tyr Phe Asp Glu Phe Thr 2255 Gly Lys 2270 Lys Arg Lys Ser Arg Arg Pro Phe 2335 Thr Ala 2350 Leu Thr Phe Tyr	Asn Glu Leu 2240 Cys Arg Asn Leu 2320 Arg Pro Leu Gln

```
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
             2405
                              2410
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
          2420
                          2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
              2440 2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
                    2455 2460
Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
                2470
                                 2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
             2485 2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
                 .
          2500
                           2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
                       2520
                                        2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
                           2540
                   2535
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
                2550 2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
                  2570
             2565
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
         2580 2585
                                           2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
   2595
                       2600
                                        2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
                    2615
                                     2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
                2630
                                 2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
             2645
                             2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile
          2660
                          2665
                                            2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
     2675 2680
                                       2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
                    2695
                                    2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
                2710
                                 2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
             2725
                              2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
          2740
                          2745
                                            2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
                       2760
                                        2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
                    2775
                                     2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
     2790
                                 2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
             2805
                             2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
                         2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
                       2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
```

	285	)				285	5				286	n			
Leu			Lvs	Tle	Gln			Phe	Glu	Glu			Gl 11	Δen	Thr
286			-7.5		2870		Olu	1110	Olu	2875		Giu	GIU	Apii	2880
		Pro	Tyr	Len			Δτα	ΔΊΞ	T.011			Gln	Gln	Wa 1	
****	шуы	110	- y -	288		DCT	Arg	Ата	289		Arg	GIII	GIII		_
λΙэ	Lau	Cln	Asp			C1.,	T 011	T			77a 7	T	7	2895	
AIA	пец	GIII	2900		Ата	GIU	пеп			Ala	val	гуѕ			Ата
7 an	Dro	7.7.			<i>α</i> 1	<b>a</b> 1	///www.	290		a1	<b>a</b> 1	<b>61</b>	2910		~ 7
Asp	PIO		Tyr	цец	GIU	GIY			ser	GIU	GIU			Arg	Ата
<b>*</b>		291			<b>~</b> 3		292	-	_	_	_	2925			
Leu			His	Arg	Gin			Asn	Asp	ьуs			Ala	GIn	Ile
	2930					293		_			2940				
		Glu	Ile	Arg			Met	Glu	Ser			Gln	Lys	Glu	Gln
294					2950	_				2955					2960
Gly	Leu	Ser	Arg			Thr	Thr	Val	${\tt Trp}$	Lys	Leu	Arg	Ile	Val	Ser
				296					2970					2975	
Tyr	Ser	Lys	Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro
			2980					298					2990		
Ser	Ser	Asp	Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile
		299					3000					3005			
Tyr	His	Leu	Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn
	3010					3015		_		_	3020		_		
Ile	Gln	Leu	Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val
3025	5				3030	) _	_			3035	5				3040
Ser	Asp	Glu	Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Ara	Glu	Pro	Leu	His
	_			3045				-	3050		5			3055	
Phe	Ser	Lvs	Phe	Leu	Asp	Pro	Asp	Phe			Ser	Cvs	Ser		
		-1	3060					3065			~~-	O _J D	3070		· u ·
Asn	Len	Tle	Gly		Val	Va l	Ser			Lare	Lare	Thr			715
		3075		1 110	vai	vai	3080		Vui	цуз	цуз	3085	_	шец	ALG
Dro	Dho		Tyr	Len	Car	λan			Ф. с.	λαn	T 011			т1.	T
110	3090		- y -	пси		3095		Cys	TYL	ASII	3100		Ата	TTE	пув
Dha			Asp	Len				Tlo	Tlo	Tara			Mot	T 011	T1.
3109		116	Asp	пеп	3110		Asp	TTE	116			HIS	мес	ьeu	
		0	7	т			70	D	<b>~</b> 1	3115		<u> </u>	~ 7	_	3120
Ата	Ата	ser	Asn			Trp	Arg	Pro			ьуs	Ser	GIY		
III la sa	T	Db	77-	3125		D)		77-7	3130				_	3135	
Thr	ьeu	Pne	Ala		Asp	Pne	Ser			Ser	Ala	Ser			Glu
<b>0</b> 1	TT -	D1	3140		m1	_,	_	3145		_	_	_,	3150		_
GTA	HIS		Gln	GIU	Thr	Pne			Met	Lys	Asn			Glu	Asn
-7	_	3155		~	_		3160		_	_	_	3165			
тте			Leu	Cys	Asn			GIu	Asn	Lys			His	Ile	Leu
•	3170					3175					3180				
		Asn	Asp	Pro			Ser	Thr	Pro			Asp	Cys	Thr	Ser
3185				_	3190					3195					3200
Gly	Pro	Tyr	Thr			Ile	Ile	Pro			Gly	Asn	Lys	Leu	Leu
				3205					3210					3215	
Met	Ser	Ser	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Leu
			3220					3225	5				3230	)	
Cys	Met	Ala	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met
		3235	5				3240	)				3245	;		
${ t Thr}$	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
	3250			-	-	3255		-			3260	_		-	
Cys	Lys	Lys	Arg	Arq	Ala			Phe	Leu	Ser			Pro	Leu	Pro
3265		-	-	~	3270		-			3275	_		-		3280
		Val	Ser	Pro			Thr	Phe	Val			Ala	Ala	Gln	
				3285		•			3290		-			3295	_
Ala	Phe	Gln	Pro			Ser	Cys	Glv			Tyr	Glu	Thr		
			3300		-		-	3305		•	-		3310		

3315	Leu Asn Sei	r Pro Gln Met Tl 3320	nr Pro Phe Lys Lys Phe 3325	
Asn Glu Ile Ser 3330	Leu Leu Glu	Ser Asn Ser I	le Ala Asp Glu Glu Leu 3340	
Ala Leu Ile Asn	Thr Gln Ala	Leu Leu Ser G	ly Ser Thr Gly Glu Lys	
3345	3350		355 3360	
Gln Phe Ile Ser	Val Ser Glu 3365	Ser Thr Arg Th	nr Ala Pro Thr Ser Ser 3375	
Glu Asp Tyr Leu 338		Arg Arg Cys Th	nr Thr Ser Leu Ile Lys 3390	
Glu Gln Glu Ser 3395	Ser Gln Ala	Ser Thr Glu G	lu Cys Glu Lys Asn Lys 3405	
Gln Asp Thr Ile 3410	Thr Thr Lys	_		
(2) IN	FORMATION FO	OR SEQ ID NO:12	:	
	NCE CHARACTE			
(A) LEN	GTH: 10485 k	ase pairs		
	E: nucleic a			
	ANDEDNESS: d OLOGY: linea			
(ii) MOLE	CULE TYPE: c	:DNA		
(ix) FEAT				
	ME/KEY: Codi	-		
	CATION: 229.	10482 TION: BRCA2 (OM)	(F)	
(2) 01		TOW DROILE (OIL	, , ,	
(xi) SEOU	ENCE DESCRIF	TION: SEQ ID NO	):12:	
,				
	CTGAAA CTAGG	CGGCA GAGGCGGAG	C CGCTGTGGCA CTGCTGCGCC	60
GGTGGCGCGA GCTT TCTGCTGCGC CTCG	GGTGTC TTTTG	CGGCG GTGGGTCGC	GC CGCTGTGGCA CTGCTGCGCC CC GCCGGGAGAA GCGTGAGGGG	60 120
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC	GGTGTC TTTTG GGCGCG GTTTT	CGGCG GTGGGTCGC	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT	120 180
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC	GGTGTC TTTTG GGCGCG GTTTT	CGGCG GTGGGTCGC	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT FT AGGTAAAA ATG CCT ATT	120
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC	GGTGTC TTTTG GGCGCG GTTTT	CGGCG GTGGGTCGC	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT	120 180
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA AGG CCA ACA	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1 CT TTT AAG ACA CGC TGC	120 180
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA AGG CCA ACA Arg Pro Thr	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1 CT TTT AAG ACA CGC TGC Le Phe Lys Thr Arg Cys	120 180 237
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA AGG CCA ACA Arg Pro Thr 10	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC  TTT TTT GAA AT Phe Phe Glu II	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  Le Phe Lys Thr Arg Cys  15	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC TTT TTT GAA AT Phe Phe Glu II	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  .e Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT	120 180 237
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC TTT TTT GAA AT Phe Phe Glu II	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  Le Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  Sn Trp Phe Glu Glu Leu	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGGA GGAATATCC  TTT TTT GAA AT Phe Phe Glu II  ATA AGT CTT AA IIle Ser Leu As	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  .e Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  sn Trp Phe Glu Glu Leu  35	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20  TCT TCA GAA GCT	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro 25	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGTCA GCAATATCC  TTT TTT GAA AT Phe Phe Glu II ATA AGT CTT AA IIle Ser Leu As 30	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  .e Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  sn Trp Phe Glu Glu Leu  35	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20  TCT TCA GAA GCT	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro 25	CGGCG GTGGGTCGC TGTCA GCTTACTCC TTGTCA GCAATATCC  TTT TTT GAA AT Phe Phe Glu II ATA AGT CTT AA IIle Ser Leu As 30	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  .e Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  sn Trp Phe Glu Glu Leu  35  CT GCA GAA GAA TCT GAA	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20  TCT TCA GAA GCT Ser Ser Glu Ala	GGTGTC TTTTG GGCGCG GTTTT TTTACC AAGCA  AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro 25  CCA CCC TAT Pro Pro Tyr 40	CCGCCG GTGGGTCGC TTGTCA GCTTACTCC TTGGA GGAATATCC TTT TTT GAA AT Phe Phe Glu II ATA AGT CTT AA Ile Ser Leu As 30 AAT TCT GAA CC Asn Ser Glu Pr	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  Le Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  EN Trp Phe Glu Glu Leu  35  CT GCA GAA GAA TCT GAA  TO Ala Glu Glu Ser Glu  50	120 180 237 285
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20  TCT TCA GAA GCT Ser Ser Glu Ala  CAT AAA AAC AAC His Lys Asn Asn	AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro 25  CCA CCC TAT Pro Pro Tyr 40  AAT TAC GAA	CCGCCG GTGGGTCGC TGTCA GCTTACTCC TTGTCA GCAATATCC  TTTT TTT GAA AT Phe Phe Glu II  ATA AGT CTT AA Ile Ser Leu As 30 AAT TCT GAA CC Asn Ser Glu Pr 45	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  Ce Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  En Trp Phe Glu Glu Leu  35  CT GCA GAA GAA TCT GAA  TO Ala Glu Glu Ser Glu  50	120 180 237 285 3333
GGTGGCGCGA GCTT TCTGCTGCGC CTCG ACAGATTTGT GACC CTGGAGCGGA CTTA  GGA TCC AAA GAG Gly Ser Lys Glu 5  AAC AAA GCA GAT Asn Lys Ala Asp 20  TCT TCA GAA GCT Ser Ser Glu Ala  CAT AAA AAC AAC	AGG CCA ACA Arg Pro Thr 10  TTA GGA CCA Leu Gly Pro 25  CCA CCC TAT Pro Pro Tyr 40  AAT TAC GAA	CCGCCG GTGGGTCGC TGTCA GCTTACTCC TTGTCA GCAATATCC  TTTT TTT GAA AT Phe Phe Glu II  ATA AGT CTT AA Ile Ser Leu As 30 AAT TCT GAA CC Asn Ser Glu Pr 45	CC GCCGGGAGAA GCGTGAGGGG CG GCCAAAAAAG AACTGCACCT ET AGGTAAAA ATG CCT ATT  Met Pro Ile  1  CT TTT AAG ACA CGC TGC  C.e Phe Lys Thr Arg Cys  15  AT TGG TTT GAA GAA CTT  EN Trp Phe Glu Glu Leu  35  CT GCA GAA GAA TCT GAA  CO Ala Glu Glu Ser Glu  50  CT AAA ACT CCA CAA AGG	120 180 237 285 3333

Lys	Pro	Ser 70	Tyr	Asn	Gln	Leu	Ala 75	Ser	Thr	Pro	Ile	Ile 80	Phe	Lys	Glu	
												AAA Lys				525
												AGT Ser				573
												GAT Asp				621
												GTT Val				669
												GTA Val 160				717
												ACA Thr				765
												ATG Met				813
												GTG Val		_	_	861
												GAT Asp				909
												CTG Leu 240				957
												ACA Thr				1005
			-									AAT Asn				1053
												CCA Pro				1101
												GAA Glu				1149

295	300	305

TCA Ser													1197
ACT Thr 325													1245
TGT Cys													1293
GAA Glu													1341
 CAG Gln													1389
CCG Pro													1437
GGA Gly 405													1485
CAA Gln													1533
AAA Lys													1581
CCA Pro	Lys	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val			1629
GAT Asp												GCA Ala	1677
AAG Lys 485													1725
 ATC Ile													1773
AAT Asn													1821

											CAT His					1869
											GAT Asp					1917
											AAG Lys 575					1965
											ATT Ile					2013
											AAA Lys		_			2061
											AAT Asn					2109
		-									TTG Leu					2157
											CCA Pro 655					2205
											TCT Ser					2253
											GAT Asp			_	_	2301
AAA Lys											ACC					2349
	Сув	ASII	695	Giu	пуѕ	пец	GIII	700	Pne	116	1111	110	705		-	
	CTG	TCA	695 TGC	CTG	CAG	GAA	GGA	700 CAG	TGT	GAA	AAT Asn	GAT	705 CCA	AAA	AGC	2397
Ser	CTG Leu	TCA Ser 710 GTT	695 TGC Cys	CTG Leu GAT	CAG Gln ATA	GAA Glu AAA	GGA Gly 715 GAA	700 CAG Gln GAG	TGT Cys GTC	GAA Glu TTG	AAT	GAT Asp 720 GCA	705 CCA Pro	AAA Lys TGT	AGC Ser	2397 2445

	_					TAT Tyr											2541
	_					GAT Asp											2589
						AAA Lys											2637
						TTA Leu											2685
I						AAT Asn 825											2733
						AGA Arg											2781
						CTA Leu											2829
						ATA Ile											2877
						AAT Asn											2925
7						AAT Asn 905											2973
						ATT Ile											3021
						CAA Gln											3069
						GAG Glu											3117
						CAA Gln											3165
G	AT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	GAC	AAA	TGG	GCA	GGA	3213

Asp 980	Lys	Ile	Pro	Glu	Lys 985	Asn	Asn	Asp	Tyr	Met 990	Asp	Lys	Trp	Ala	Gly 995	
			Pro		TCA Ser			Ser					Phe			3261
_		Asn			ATC Ile		Leu				_	Ile				3309
	Met				GAT Asp	Ile					Pro					3357
Cys					AAT Asn					Asp						3405
				Ser	ATT Ile 1065				Ser					Ser		3453
			Ser		TGT Cys			Ser					${\tt Gln}$			3501
		Lys			TTT Phe		Ser					Thr				3549
					GAA Glu											3597
		110				1	.115			Бец		120	DCI	2	501	
Gln	TTT	GAA	TTT		CAG Gln	TTT	.115 AGA		CCA	AGC Ser	TAC	ATA	TTG	CAG	AAG	3645
Gln : AGT	TTT Phe 1125 ACA	GAA Glu TTT	TTT Phe GAA	Thr GTG Val	Gln	TTT Phe 130	AGA Arg	Lys	CCA Pro ATG Met	AGC Ser 1	TAC Tyr 135 ATC	ATA Ile TTA	TTG Leu AAG	CAG Gln ACC Thr	AAG Lys ACT	3645 3693
Gln AGT Ser 1140 TCT	TTT Phe 1125 ACA Thr	GAA Glu TTT Phe	TTT Phe GAA Glu TGC Cys	Thr GTG Val AGA	Gln CCT Pro	TTT Phe 130 GAA Glu GCT	AGA Arg AAC Asn	CAG Gln CTT Leu	CCA Pro ATG Met	AGC Ser 1 ACT Thr 150	TAC Tyr 135 ATC Ile	ATA Ile TTA Leu	TTG Leu AAG Lys AAT Asn	CAG Gln ACC Thr	AAG Lys ACT Thr 155	
Gln AGT Ser 1140 TCT Ser TCG	TTT Phe 125 ACA Thr GAG Glu	GAA Glu TTT Phe GAA Glu GGT Gly	TTT Phe GAA Glu TGC Cys	Thr  GTG Val  AGA Arg	Gln CCT Pro 1145 GAT	TTT Phe 130 GAA Glu GCT Ala	AGA AAC ASN GAT ASP	Lys CAG Gln CTT Leu 1	CCA Pro  ATG Met  CAT His	AGC Ser 1 ACT Thr 150 GTC Val	TAC Tyr 135 ATC Ile ATA Ile	ATA Ile  TTA Leu  ATG Met  GGT Gly	TTG Leu AAG Lys AAT Asn	CAG Gln ACC Thr 1 GCC Ala 170	AAG Lys ACT Thr 155 CCA Pro	3693
Gln AGT Ser 1140 TCT Ser TCG Ser	TTT Phe 1125 ACA Thr GAG Glu ATT Ile	GAA Glu TTT Phe GAA Glu GGT Gly 1	TTT Phe GAA Glu TGC Cys CAG Gln 175	Thr  GTG Val  AGA Arg 160 GTA Val	Gln CCT Pro 1145 GAT Asp	TTT Phe .130 GAA Glu GCT Ala AGC Ser GGC Gly	AGA Arg  AAC Asn  GAT Asp  AGC Ser  1	CAG Gln CTT Leu 1 AAG Lys 180	CCA Pro  ATG Met  CAT His 165 CAA Gln	AGC Ser 1 ACT Thr 150 GTC Val TTT Phe	TAC Tyr 135 ATC Ile ATA Ile GAA Glu GAC Asp	ATA Ile  TTA Leu  ATG Met  GGT Gly TGT	TTG Leu AAG Lys AAT Asn ACA Thr 185	CAG Gln ACC Thr GCC Ala 170 GTT Val	AAG Lys ACT Thr 155 CCA Pro GAA Glu	3693 3741

1205 1210 1215

				T ACT GAA GCT C r Thr Glu Ala L 0	
		Phe Ser As		T ATT AGT GAG G n Ile Ser Glu G 12	
				A AGT AAA TGT C r Ser Lys Cys H 1265	
Ser Val			le Glu Asn Hi	T AAT GAT AAA A s Asn Asp Lys T 1280	
				A CAA AAT AAT A u Gln Asn Asn I 1295	
				T GAA AAT TAC A ur Glu Asn Tyr L .0	
		ı Asp Asn Ly		T GCC AGT AGA A a Ala Ser Arg A 13	
				T AAA AAT GAT A er Lys Asn Asp T 1345	
Cys Ile			sp Leu Leu Ph	T ACT GAT CAG C ne Thr Asp Gln H 1360	
	Leu Lys Le	ser Gly G		AG GAG GGA AAC A rs Glu Gly Asn T 1375	
				CG GAA GTT GCG A eu Glu Val Ala I 90	
		s Gly Asn T		AA GAA CAG TTA A 's Glu Gln Leu T 14	
					CA TTT 4509
	ACG GAG CAA Thr Glu Gli 1415			u Thr Ser Asp T	

AAT AAA ATT GTA Asn Lys Ile Val 1445		Glu Leu His Asn	4605
TTT TCC TTA AAT Phe Ser Leu Asn 1460		<del>-</del>	4653
GAC ATT CTA AGT Asp Ile Leu Ser 1			4701
AAA GAA AGT GTC Lys Glu Ser Val 1495			4749
GGA CAA CCC GAA Gly Gln Pro Glu 1510	Ile Lys Glu Pro		4797
TTT CAT ACA GCT Phe His Thr Ala 1525			4845
GAC AAA GTG AAA Asp Lys Val Lys 1540			4893
		AAG TAC AGA GAG Lys Tyr Arg Glu 1570	4941
GCC TGT AAA GAC Ala Cys Lys Asp 1575			4989
GCC CCA AAG TGT Ala Pro Lys Cys 1590	Asn Ser Leu Asn		5037
CTT GTT TCT ATT Leu Val Ser Ile 1605			5085
TTA TGT AGA CAA Leu Cys Arg Gln 1620			5133
AAA GTT AAA GTA Lys Val Lys Val 1			5181
GCA ACT TGT TAC Ala Thr Cys Tyr 1655		ATT GAA AAT TCA Ile Glu Asn Ser	5229

	Leu	GCT Ala 1670				Ser					Thr					5277
Thr		TTA Leu			Ala					Arg						5325
		CCA Pro		Arg					Asp					Tyr		5373
		AAT Asn	Asn					Ile					Lys			5421
		GAA Glu					Tyr					Ser				5469
	Tyr	TCC Ser 1750				Asp		-			Asp					5517
Ser		AAT Asn			Asp					Pro						5565
		CAA Gln		Asn					Lys					Val		5613
		AAT Asn	Ala					Val					Cys			5661
		GTG Val					Pro					Asn				5709
	Leu	TCC Ser 1830				Ser					Val					5757
Phe		ATA Ile			Gly					Val						5805
		GTG Val		Asp					Ser					Ile		5853
		AAC Asn	Glu					Ile					Ile			5901
GGT	TGT	TAC	GAG	GCA	TTG	GAT	GAT	TCA	GAG	GAT	ATT	CTT	CAT	AAC	TCT	5949

Gly	Сув	-	Glu 1895	Ala	Leu	Asp		Ser 1900	Glu	Asp	Ile		His L905	Asn	Ser	
	Asp				TGT Cys	Ser					Lys					5997
Ile					ATT Ile					Gln						6045
				Lys	ATA Ile 1945				Asp					Thr		6093
			Lys		AGT Ser			Lys					Val			6141
		Thr			ATT Ile		Ser					Lys				6189
	Ser				TTA Leu	Gln					Val					6237
Glu					CAA Gln					Val						6285
				Gln	CTC Leu 2025				Glu					Arg		6333
			Leu		TCC Ser			Gly					Val			6381
		Ala			GGA Gly		Ser					Lys				6429
	Leu				TTA Leu	His					Val					6477
Asp					GAG Glu					Tyr						6525
				Lys	ATA Ile 2105				Val					Pro		6573
CAC																6621

			;	2120				7	2125				:	2130		
		AAT														6669
Leu	Ser	Asn	Asn 2135	Leu	Asn	Val		Gly 2140	Gly	Ser	Ser		Asn 2145	Asn	His	
	3 000				~~~				<b></b>		~				~~~	
		AAA Lys														6717
	:	2150				2	2155				2	2160				
		GTA														6765
	Leu 2165	Val	Leu	Gly		Lys 2170	Val	Ser	Leu		Glu 2175	Asn	Ile	His	Val	
		AAA Lys														6813
2180	-	•			2185			•		2190	•				2195	
AAA	ACT	GAA	ACT	TTT	TCT	GAT	GTT	CCT	GTG	AAA	ACA	AAT	ATA	GAA	GTT	6861
Lys	Thr	Glu		Phe 2200	Ser	Asp	Val		Val 2205	Lys	Thr	Asn		Glu 2210	Val	
		ACT Thr														6909
Cyb	501		2215	501	шуы	nop		2220	non	- 7 -	1110		2225	Olu	AIU	
GTA	GAA	ATT	GCT	AAA	GCT	ттт	ATG	GAA	GAT	GAT	GAA	CTG	ACA	GAT	TCT	6957
Val		Ile	Ala	Lys	Ala			Glu	Asp	Asp			Thr	Asp	Ser	
		2230				2	2235				2	2240				
		CCA Pro														7005
_	2245	PIO	per	uis		2250	птв	ser	ьеи		2255	Суѕ	PIO	GIU	ASII	
GAG	GAA	ATG	GTT	TTG	тса	ΔΔΤ	тса	AGA	ΔТТ	GGA	ααα	AGA	AGA	GGA	GAG	7053
Glu		Met							Ile	Gly						, 033
2260				2	2265				2	2270				7	2275	
		ATC														7101
Pro	ьеи	Ile		Val 2280	GIY	Glu	Pro		11e 2285	гуs	Arg	Asn		ьеи 2290	Asn	
<i>(</i> , , , , , , , , , , , , , , , , , , ,	mmm	a	7.00	7 173 7	202	<b>C N N</b>	7 7 C	<b>CIA</b> A	<b>~</b> ~ ~ ~		maa	CCC 2	7 7 C	aam	man	77.40
		GAC Asp				_		_	-							7149
		2	2295				2	2300				2	2305			
		ACT														7197
ГЛЗ		Thr 2310	Pro	Asp	Gly		Ile 2315	Lys	Asp	Arg	_	Leu 2320	Phe	Met	His	
_																
		TCT Ser														7245
	2225		<del>-</del>	<del>_</del>		227		2			2225				4 -	

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA

Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu

	CTG Leu		Lys					Glu					Glu		7341
	AGC Ser	Asn					Gly					Gln			7389
	AGA Arg					Arg					Thr				7437
Lys	GTC Val 2405				Pro					Ser					7485
	CAG Gln			Arg					Glu					Lys	7533
	ATT Ile		Gly					Asp					Ile		7581
	GAG Glu	Ile					Lys					Gln			7629
	ACT Thr					Glu					Asp				7677
Leu	CAG Gln 2485				Asp					Arg					7725
Arg	CAA Gln	Arg	Val	Phe		Gln	Pro	Gly	Ser		Tyr	Leu	Ala	Lys	7773
	ACT Thr		Pro					Lys					Gly		7821
	TCT Ser	Ala					Gln					Gly			7869
	TGC Cys					Ser					Ser				7917
	GAA Glu 2565				Gly					Trp					7965

CAG Gln 2580				Gly					Pro					Lys		8013
GGA Gly			Glu					Leu					Gly			8061
CCA Pro		Leu					${\tt Trp}$					Tyr				8109
ATA Ile	Trp					Met					Pro					8157
AAT Asn 2					Pro					Leu						8205
TAT Tyr 2660				Ile					Arg					Lys		8253
ATG Met			Asp					Lys					Cys			8301
GAC Asp		Ile					Asn					Ser				8349
ACT Thr	Ser					Gln					Ile					8397
GGG Gly 2					Lys					Pro						8445
TTA . Leu 2740				Arg					Gln					His		8493
GCA Ala			Val					Ala					Glu			8541
GAA Glu		Leu					Ser					Arg				8589
TGG Trp	Tyr					Phe					Arg					8637
CCC	TTA	TCA	TCG	CTT	TTC	AGT	GAT	GGA	GGA	AAT	GTT	GGT	TGT	GTT	GAT	8685

	eu Ser 05	Ser	Leu		Ser 2810	Asp	Gly	Gly		Val 2815	Gly	Cys	Val	Asp	
	TT ATT		Arg					Gln					Thr		8733
	GA TTA	Tyr					Glu					Lys			8781
	AA TAT ys Tyr					Gln					Ala				8829
	TT CAG le Gln 2870	Glu			Glu					Asn					8877
Tyr L	TA CCA eu Pro 85			Ala					Gln						8925
	GT GCA		Leụ					Lys					Pro		8973
	TT GAG eu Glu	Gly					Glu					Leu			9021
_	GG CAA rg Gln					Lys					Ile				9069
	GG AAG rg Lys 2950	Thr			Ser					Glu					9117
	AT GTC sp Val 65			Val					Ile						9165
	AA AAA lu Lys		Ser					Ile					Ser		9213
	AT TCT yr Ser	Leu					Lys					Tyr			9261
	CT TCA hr Ser					Lys					Asn				9309
	CG ACA la Thr														9357

3030 3035 3040

3.00			~~~													
	TTA Leu															9405
	3045					3050		5			3055				_, _	
הרוים	TTA	САТ	CCA	GAC	արար	CAG	CCA	тст	ጥርም	тст	GAG	стс	GNG	CTTA	א ידי א	9453
	Leu															9453
3060				_ :	3065					3070			-	;	3075	
GGA	TTT	GTC	GTT	TCT	GTT	GTG	AAA	AAA	ACA	GGA	СТТ	GCC	ССТ	ттс	GTC	9501
	Phe															JJ01
			3	3080				:	3085				;	3090		
TAT	TTG	TCA	GAC	GAA	TGT	TAC	AAT	TTA	CTG	GCA	ATA	AAG	TTT	TGG	ATA	9549
Tyr	Leu			Glu	Cys	Tyr			Leu	Ala	Ile	_		Trp	Ile	
		3	3095					3100				:	3105			
GAC	CTT	AAT	GAG	GAC	ATT	ATT	AAG	CCT	CAT	ATG	TTA	ATT	GCT	GCA	AGC	9597
Asp	Leu		Glu	Asp	Ile		-	Pro	His	Met			Ala	Ala	Ser	
	•	3110				3	3115				3	3120				
AAC	CTC	CAG	TGG	CGA	CCA	GAA	TCC	AAA	TCA	GGC	CTT	CTT	ACT	TTA	TTT	9645
	Leu	Gln	Trp	Arg			Ser	Lys	Ser	_		Leu	Thr	Leu	Phe	
•	3125				-	3130				4	3135					
	GGA															9693
	Gly	Asp	Phe			Phe	Ser	Ala			Lys	Glu	Gly			
3140				-	3145				4	3150				-	3155	
	GAG															9741
Gln	Glu	Thr		Asn 3160	Lys	Met	Lys		Thr 3165	Val	Glu	Asn		Asp 3170	Ile	
			-	,100					,105				-	3170		
	TGC															9789
Leu	Cys		Glu 3175	Ala	Glu	Asn	_	Leu 3180	Met	His	Ile		His 3185	Ala	Asn	
		-	,1,5				`	,100				-	,105			
	CCC															9837
Asp	Pro				Thr									Pro	Tyr	
	•	, 130				_	,1,5				•	200				
	GCT															9885
	Ala 3205	GIN	ше	шe		GIY 3210	Thr	GIA	Asn	_	Leu 3215	Leu	Met	Ser	Ser	
	TAA															9933
3220	Asn	Cys	GIU		3225	TYL	GIII	ser		ьец 3230	ser	Leu	Cys		A1a 3235	
	_															
	AGG Arg															9981
y ⊳	Ar 9	пур		3240	Set	TIIL	FIO		3245	міа	3111	MEL		3250	пур	
m-~-	mc=	777	aca	~~		a	3 CC	<b></b>	a. ~	a			mc -			
	TGT Cys															10029
	- 1 -		255		_1 ~			3260	<b>P</b>		- <i>1</i> •		3265	_, •	_, 5	

		GCC														10077
Arg		Ala 3270	Leu	Asp	Pne		Ser 3275	Arg	ьeu	Pro		Pro 3280	Pro	Pro	Val	
		52,0				•	12/5				•	3200				
		ATT														10125
		Ile	Cys	Thr			Ser	Pro	Ala			Lys	Ala	Phe	Gln	
•	3285					3290				:	3295					
CCA	CCA	AGG	AGT	TGT	GGC	ACC	AAA	TAC	GAA	ACA	CCC	АТА	AAG	AAA	AAA	10173
		Arg														
3300				:	3305				:	3310				:	3315	
מאא	CTC	א א ידי	man	COM	ana	N TO CT	» CID	aa.	mmm	777		mma		<b>a.</b>	3 mm	
		AAT Asn														10221
				3320	<b>U</b>				3325	ביים	Буб	1110		3330	110	
		TTG														10269
Ser	Leu	Leu	G1u 3335	Ser	Asn	Ser		A1a 3340	Asp	Glu	Glu			Leu	Ile	
		_	,,,,				-	340				-	3345			
AAT	ACC	CAA	GCT	CTT	TTG	TCT	GGT	TCA	ACA	GGA	GAA	AAA	CAA	TTT	ATA	10317
Asn		Gln	Ala	Leu	Leu			Ser	Thr	Gly	Glu	Lys	Gln	Phe	Ile	
	3	3350				3	355				3	3360				
тст	GTC	AGT	GAA	TCC	ACT	AGG	АСТ	GCT	CCC	ACC	ΔGT	тса	GDD	СУТ	тдт	10365
		Ser														10303
	3365					370					3375			-	•	
СПС	7 (7 7	ата	***	GG 7	OO.	mam	7 CM	202	mam	ama.			~	~~~		
		CTG Leu														10413
3380	9	<b></b>	_,0		3385	Cyb	1111	****		3390	110	пуъ	Giu		3395	
		CAG														10461
Ser	ser	Gln		Ser 400	Thr	Glu	GIu		G1u 3405	Lys	Asn	Lys		_	Thr	
			3	400				4	405				-	3410		
ATT	ACA	ACT	AAA	AAA	TAT	ATC	TAA									10485
Ile	Thr	Thr		Lys	Tyr	Ile										
		3	415													

# (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 1 5 10 15

```
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
                                        75
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
                                    90
                85
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
            100
                                105
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
                            120
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
                        135
                                            140
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
                   150
                                        155
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
               165
                                    170
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
           180
                               185
Ser Trp Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                            200
       195
                                                205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                        215
                                            220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                    230
                                        235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                245
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
                                265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                            280
His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                        295
                                            300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                        315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                325
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                        395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
               405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
           420
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
```

```
475
465
                    470
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
                                                525
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                       555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                    570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                            600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                        615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                    630
                                        635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                645
                                    650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
                                665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                            680
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                   710
                                        715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
                                    730
               725
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
                                745
            740
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
                                                765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
                805
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
                                825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
                                                845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
                                            860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn
                885
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
        915
                            920
```

```
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                     935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                  950
                                    955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
              965
                                970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
           980
                            985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
       995
                         1000
                                           1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                     1015
                                        1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                  1030
                                   1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
              1045
                               1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
          1060
                            1065
                                    1070
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
               1080
                              1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
    1090 1095
                           1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                 1110
                                   1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
              1125
                                1130
                                                  1135
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
           1140
                            1145
                                              1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
                         1160
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                    1175
                                       1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                 1190
                                   1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
                    1210
              1205
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
          1220
                           1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
       1235
                        1240
                                           1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                     1255
                                       1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                  1270
                                   1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
              1285
                               1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
                            1305
                                             1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                        1320 1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                     1335
                                      1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                1350
                                  1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
              1365
                                1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
```

	1380				1385	5				1390	)	
Ala Lys Al 13	a Gln 95	Glu Ala	Cys	His 1400		Asn	Thr	Ser	Asn 1405	_	Glu	Gln
Leu Thr Al 1410	a Thr	Lys Thr	Glu 1415	Gln		Ile	Lys	Asp 1420		Glu	Thr	Ser
Asp Thr Ph 1425	e Phe	Gln Thr 143		Ser	Gly	Lys	Asn 1435		Ser	Val	Ala	Lys 1440
Glu Ser Ph		Lys Ile 1445	Val	Asn	Phe	Phe 1450	_	Gln	Lys	Pro	Glu 1455	
Leu His As	n Phe 1460		Asn	Ser	Glu 1465		His	Ser	Asp	Ile 1470	-	Lys
	75			1480	)			_	1485	5	_	
Lys Ile Le 1490	_		1495	5		_		1500	)			
Thr Phe Gl 1505		151	0				1515	5	_			1520
Leu Leu Gl		1525				1530	)				1535	5
Glu Ser Le	1540	_	_		1545	5	_		_	1550	)	_
Thr Ser Gl	55			1560	)		_		1565	i		=
Tyr Arg Gl 1570			1575	5				1580	)			
Ile Thr Al		159	0	_			1595	;				1600
Asp Lys As		1605	ше	GIU	inr	vai 1610		Pro		гла	ьеи 1615	
Ser Asp As	n Leu 1620		Gln	Thr	Glu 1625		Leu	Lys	Thr	Ser 1630	_	Ser
Ser Asp As Ile Phe Le	1620 u Lys				1625 Glu	5		-		1630 Glu	)	
Ile Phe Le	1620 u Lys 35	Val Lys	Val	His 1640 Thr	1625 Glu )	Asn	Val	Glu	Lys 1645 Tyr	1630 Glu	Thr	Ala
Ile Phe Le 16 Lys Ser Pr	1620 u Lys 35 o Ala	Val Lys Thr Cys	Val Tyr 1655 Phe	His 1640 Thr	1625 Glu ) Asn	Asn Gln	Val Ser	Glu Pro 1660 Ser	Lys 1645 Tyr	1630 Glu Ser	Thr Val	Ala Ile
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se	1620 u Lys 35 o Ala r Ala	Val Lys Thr Cys Leu Ala 167	Val Tyr 1655 Phe 0	His 1640 Thr Tyr	1625 Glu ) Asn Thr	Asn Gln Ser	Val Ser Cys 1675 Lys	Glu Pro 1660 Ser	Lys 1645 Tyr ) Arg	1630 Glu Ser Lys	Thr Val	Ala Ile Ser 1680 Gly
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665	1620 u Lys 35 o Ala r Ala	Val Lys Thr Cys Leu Ala 1670 Ser Leu 1685	Val Tyr 1655 Phe O Leu	His 1640 Thr Tyr	1625 Glu Asn Thr	Asn Gln Ser Lys 1690 Asn	Val Ser Cys 1675 Lys	Glu Pro 1660 Ser Trp	Lys 1645 Tyr Arg Leu	1630 Glu Ser Lys Arg	Thr Val Thr Glu 1695 Val	Ala Ile Ser 1680 Gly
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr	Val Lys Thr Cys Leu Ala 167 Ser Leu 1685 Gln Pro Glu Asn	Val Tyr 1655 Phe O Leu Glu	His 1640 Thr Tyr Glu Arg Ser 1720	1625 Glu Asn Thr Ala Ile 1705 Asn	Asn Gln Ser Lys 1690 Asn Ser	Val Ser Cys 1675 Lys Thr	Glu Pro 1660 Ser Trp Ala Ile	Lys 1645 Tyr Arg Leu Asp Ala 1725	1630 Glu Ser Lys Arg Tyr 1710 Glu	Thr Val Thr Glu 1695 Val Asn	Ala Ile Ser 1680 Gly Gly Asp
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu	Val Lys Thr Cys Leu Ala 167 Ser Leu 1685 Gln Pro Glu Asn Ser Glu	Val Tyr 1655 Phe 0 Leu Glu Asn Lys 1735	His 1640 Thr Tyr Glu Arg Ser 1720 Gln	1625 Glu Asn Thr Ala Ile 1705 Asn	Asn Gln Ser Lys 1690 Asn Ser	Val Ser Cys 1675 Lys Thr Thr	Glu Pro 1660 Ser Trp Ala Ile Leu 1740	Lys 1645 Tyr Arg Leu Asp Ala 1725 Ser	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn	Thr Val Thr Glu 1695 Val Asn	Ala Ile Ser 1680 Gly Gly Asp Ser
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730 Met Ser As 1745	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu n Ser	Val Lys Thr Cys Leu Ala 1670 Ser Leu 1685 Gln Pro Glu Asn Ser Glu Tyr Ser	Val Tyr 1655 Phe Clu Glu Asn Lys 1735 Tyr	His 1640 Thr Tyr Glu Arg Ser 1720 Gln	1625 Glu Asn Thr Ala Ile 1705 Asn Asp	Asn Gln Ser Lys 1690 Asn Ser Thr	Val Ser Cys 1675 Lys Thr Thr Tyr Glu 1755	Glu Pro 1660 Ser Trp Ala Ile Leu 1740 Val	Lys 1645 Tyr Arg Leu Asp Ala 1725 Ser	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn	Thr Val Thr Glu 1695 Val Asn Ser	Ala Ile Ser 1680 Gly Gly Asp Ser Ser 1760
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730 Met Ser As 1745 Gly Tyr Le	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu n Ser	Val Lys Thr Cys Leu Ala 1670 Ser Leu 1685 Gln Pro Glu Asn Ser Glu Tyr Ser 1750 Lys Asn	Val Tyr 1655 Phe 0 Leu Glu Asn Lys 1735 Tyr 0 Lys	His 1640 Thr Tyr Glu Arg Ser 1720 Gln His Leu	Asn Thr Ala Ile 1705 Asn Asp Ser Asp	Asn Gln Ser Lys 1690 Asn Ser Thr Asp Ser 1770	Val Ser Cys 1675 Lys Thr Thr Glu 1755 Gly	Glu Pro 1660 Ser Trp Ala Ile Leu 1740 Val	Lys 1645 Tyr Arg Leu Asp Ala 1725 Ser Tyr	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn Asn	Thr Val Thr Glu 1695 Val Asn Ser Asp	Ala Ile Ser 1680 Gly Gly Asp Ser Ser 1760 Leu
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730 Met Ser As 1745 Gly Tyr Le	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu u Ser u Ser 1 Glu 1780	Val Lys Thr Cys Leu Ala 1670 Ser Leu 1685 Gln Pro Glu Asn Ser Glu Tyr Ser 1750 Lys Asn 1765 Asp Gln	Val Tyr 1655 Phe 0 Leu Glu Asn Lys 1735 Tyr 0 Lys	His 1640 Thr Tyr Glu Arg Ser 1720 Gln His Leu	Asn Thr Ala Ile 1705 Asn Asp Ser Asp	Asn Gln Ser Lys 1690 Asn Ser Thr Asp Ser 1770 Ser	Val Ser Cys 1675 Lys Thr Thr Glu 1755 Gly Phe	Glu Pro 1660 Ser Trp Ala Ile Leu 1740 Val Ile Ser	Lys 1645 Tyr  Arg Leu Asp Ala 1725 Ser Tyr Glu Lys	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn Pro Val	Thr Val Thr Glu 1695 Val Asn Ser Asp Val 1775 Ile	Ala Ile Ser 1680 Gly Gly Asp Ser 1760 Leu Ser
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730 Met Ser As 1745 Gly Tyr Le Lys Asn Val Asn Val Ly	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu n Ser u Ser 1780 s Asp	Val Lys Thr Cys Leu Ala 1676 Ser Leu 1685 Gln Pro Glu Asn Ser Glu Tyr Ser 1756 Lys Asn 1765 Asp Gln Ala Asn	Val Tyr 1655 Phe 0 Leu Glu Asn Lys 1735 Tyr 0 Lys Lys	His 1640 Thr Tyr Glu Arg Ser 1720 Gln His Leu Asn	Asn Thr Ala Ile 1705 Asn Asp Ser Asp Thr 1785	Asn Gln Ser Lys 1690 Asn Ser Thr Asp Ser 1770 Ser Gln	Val Ser Cys 1675 Lys Thr Thr Tyr Glu 1755 Gly Phe	Glu Pro 1660 Ser Trp Ala Ile Leu 1740 Val Ile Ser Val	Lys 1645 Tyr Arg Leu Asp Ala 1725 Ser Tyr Glu Lys Asn 1805	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn Pro Val 1790 Glu	Thr Val Thr Glu 1695 Val Asn Ser Asp Val 1775 Ile	Ala Ile Ser 1680 Gly Gly Asp Ser 1760 Leu Ser Ile
Ile Phe Le 16 Lys Ser Pr 1650 Glu Asn Se 1665 Val Ser Gl Ile Phe As Asn Tyr Le 17 Lys Asn Hi 1730 Met Ser As 1745 Gly Tyr Le Lys Asn Val	1620 u Lys 35 o Ala r Ala n Thr 1700 u Tyr 15 s Leu u Ser u Ser 1780 s Asp 95 u Glu	Val Lys Thr Cys Leu Ala 167 Ser Leu 1685 Gln Pro Glu Asn Ser Glu Tyr Ser 1755 Lys Asn 1765 Asp Gln Ala Asn Leu Val	Val Tyr 1655 Phe 0 Leu Glu Asn Lys 1735 Tyr 0 Lys Lys Ala Thr 1815	His 1640 Thr Glu Arg Ser 1720 Gln His Leu Asn Tyr 1800 Ser	Asn Thr Ala Ile 1705 Asn Asp Ser Asp Thr 1785 Pro	Asn Gln Ser Lys 1690 Asn Ser Thr Asp Ser 1770 Ser Gln Ser	Val Ser Cys 1675 Lys Thr Thr Tyr Glu 1755 Gly Phe Thr	Glu Pro 1660 Ser Trp Ala Ile Leu 1740 Val Ile Ser Val Cys 1820	Lys 1645 Tyr Arg Leu Asp Ala 1725 Ser Tyr Glu Lys Asn 1805 Lys	1630 Glu Ser Lys Arg Tyr 1710 Glu Asn Pro Val 1790 Glu Asn	Thr Val Thr Glu 1695 Val Asn Ser Asp Val 1775 Ile Asp	Ala Ile Ser 1680 Gly Gly Asp Ser 1760 Leu Ser Ile Asn

```
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
                                1850
              1845
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
          1860
                            1865
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
                                           1885
                         1880
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                     1895
                             1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                  1910 1915 1920
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
                                 1930
              1925
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
                             1945
                                               1950
           1940
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                                            1965
                         1960
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
                     1975
                                        1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
           1990
                         1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
              2005
                                2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
           2020
                             2025
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
                                            2045
                         2040
       2035
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                      2055
                                         2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                                    2075
                  2070
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
                                 2090
              2085
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
           2100 2105
                                                2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
                         2120
                                            2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                      2135
                                        2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                  2150
                                     2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
                                 2170
              2165
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
                             2185
                                               2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
       2195
                                            2205
                         2200
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
                      2215 2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                                    2235
                  2230
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
                                 2250
               2245
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
                                                2270
           2260
                              2265
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
                          2280
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
```

2290		2295			2	2300				
Lys Ala Ser Ly 2305	s Ser Thr 2310		p Gly		Ile I 2315	уs	Asp	Arg		Leu 2320
Phe Met His Hi	s Val Ser 2325	Leu Glu		Ile 3 2330	Thr (	Cys	Val	Pro	Phe 2335	
Thr Thr Lys Gl 23	u Arg Gln 40	Glu Ile	e Gln 2345		Pro <i>P</i>	Asn		Thr 2350		Pro
Gly Gln Glu Ph 2355	e Leu Ser	Lys Ser		Leu '	Tyr (		His 2365		Thr	Leu
Glu Lys Ser Se 2370		2375			2	2380				
Val Ser Ala Th 2385	239	0			2395					2400
Arg Pro Thr Ly	2405			2410					2415	;
	20		2425	5				2430	1	
Gln Lys Gln As 2435		24	40				2445	;		
Ile Asn Asp As 2450		2455			2	2460				
Ala Ala Ala Va 2465	247	0		;	2475					2480
Ile Thr Ser Le	2485			2490					2495	5
	00		2505	5				2510	)	
Ala Lys Thr Se 2515		25	20				2525	;		
Gly Gln Val Pr 2530		2535				2540				
2530 Val Ser Lys Hi 2545	s Cys Ile 255	2535 Lys Il 0	e Asn	Ser	Lys <i>1</i> 2555	2540 Asn	Ala	Glu	Ser	Phe 2560
2530 Val Ser Lys Hi 2545 Gln Phe His Th	s Cys Ile 255 ir Glu Asp 2565	2535 Lys Il 0 Tyr Ph	e Asn e Gly	Ser Lys 2570	Lys 1 2555 Glu S	2540 Asn Ser	Ala Leu	Glu Trp	Ser Thr 2575	Phe 2560 Gly
2530 Val Ser Lys Hi 2545 Gln Phe His Th Lys Gly Ile Gl	s Cys Ile 255 r Glu Asp 2565 n Leu Ala	2535 Lys Ilo O Tyr Pho Asp Gl	e Asn e Gly y Gly 2585	Ser Lys 2570 Trp	Lys 1 2555 Glu s Leu I	2540 Asn Ser Ile	Ala Leu Pro	Glu Trp Ser 2590	Ser Thr 2575 Asn	Phe 2560 Gly Asp
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595	s Cys Ile 255 r Glu Asp 2565 n Leu Ala 880 y Lys Glu	2535 Lys Ile 0 Tyr Phe Asp Gl Glu Phe 26	e Asn e Gly y Gly 2585 e Tyr	Ser Lys 2570 Trp Arg	Lys A 2555 Glu S Leu I	2540 Asn Ser Ile Leu	Ala Leu Pro Cys 2605	Glu Trp Ser 2590 Asp	Ser Thr 2575 Asn ) Thr	Phe 2560 Gly Asp Pro
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610	s Cys Ile 255 r Glu Asp 2565 n Leu Ala 80 ry Lys Glu	2535 Lys Ile  Tyr Phe Asp Gl: Glu Phe 26 Ile Se 2615	e Asn e Gly y Gly 2585 e Tyr 00 r Arg	Ser Lys 2570 Trp Arg	Lys 1 2555 Glu s Leu : Ala l	2540 Asn Ser Ile Leu Val 2620	Ala Leu Pro Cys 2605 Tyr	Glu Trp Ser 2590 Asp Asn	Thr 2575 Asn Thr	Phe 2560 Gly Asp Pro
2530 Val Ser Lys Hi 2545 Gln Phe His Th Lys Gly Ile Gl 25 Gly Lys Ala Gl 2595 Gly Val Asp Pr	s Cys Ile 255 r Glu Asp 2565 n Leu Ala 80 ry Lys Glu	2535 Lys Ilo O Tyr Pho Asp Gl; Glu Pho 26 Ile Se 2615 Leu Al	e Asn e Gly y Gly 2585 e Tyr 00 r Arg	Ser Lys 2570 Trp Arg Ile	Lys 1 2555 Glu s Leu : Ala l	2540 Asn Ser Ile Leu Val 2620	Ala Leu Pro Cys 2605 Tyr	Glu Trp Ser 2590 Asp Asn	Thr 2575 Asn Thr	Phe 2560 Gly Asp Pro
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu To Lys Leu Le Trp Lys 263 In Arg Cys 2645	2535 Lys Ile  Tyr Phe Asp Gl: Glu Phe 26 Ile Se: 2615 Leu Al: 0 Leu Se	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro	Lys 2570 Trp Arg Ile Met Glu 2650	Lys A 2555 Glu S Leu : Ala I Trp S Glu G 2635 Arg S	2540 Asn Ser Ile Leu Val 2620 Cys	Ala Leu Pro Cys 2605 Tyr Ala Leu	Glu Trp Ser 2590 Asp Asn Phe Leu	Thr 2575 Asn Thr His Pro Gln 2655	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As  Lys Tyr Arg Ty 26	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu Io Lys Leu Ie Trp Lys 263 In Arg Cys 2645 Ir Asp Thr	2535 Lys Ile  Tyr Phe Asp Gl; Glu Phe 26 Ile Se 2615 Leu Al  Leu Se Glu Il	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro e Asp 2665	Ser Lys 2570 Trp Arg Ile Met Glu 2650 Arg	Lys A 2555 Glu S Leu : Ala I Trp : Glu G 2635 Arg : Ser A	2540 Asn Ser Ile Leu Val 2620 Cys Val	Ala Leu Pro Cys 2605 Tyr Ala Leu	Glu Trp Ser 2590 Asp Asn Phe Leu Ser 2670	Thr 2575 Asn Thr His Pro Gln 2655 Ala	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu Ile
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As  Lys Tyr Arg Ty 26  Lys Lys Ile Me 2675	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu Io Lys Leu Ie Trp Lys 263 In Arg Cys 2645 Ir Asp Thr 660 Iet Glu Arg	2535 Lys Ile  Tyr Phe Asp Gl; Glu Phe 26 Ile Se 2615 Leu Al: 0 Leu Se Glu Il Asp As; 26	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro e Asp 2665 p Thr	Ser Lys 2570 Trp Arg Ile Met Glu 2650 Arg Ala	Lys A 2555 Glu S Leu : Ala : Trp S Glu G 2635 Arg S Ser A	2540 Asn Ser Ile Leu Val 2620 Cys Val Arg	Ala Leu Pro Cys 2605 Tyr Ala Leu Arg	Glu Trp Ser 2590 Asp Asn Phe Leu Ser 2670 Leu	Thr 2575 Asn Thr His Pro Gln 2655 Ala	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu Ile Leu
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As  Lys Tyr Arg Ty 26  Lys Lys Ile Me 2675  Cys Val Ser As 2690	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu Io Lys Leu Ie Trp Lys 263 In Arg Cys 2645 Ir Asp Thr 60 Iet Glu Arg	2535 Lys Ile  Tyr Phe Asp Gl  Glu Phe 26 Ile Se 2615 Leu Al  Leu Se Glu Il  Asp As 26 Ser Le 2695	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro e Asp 2665 p Thr 80 u Ser	Lys 2570 Trp Arg Ile Met Clu 2650 Arg Ala	Lys A 2555 Glu S Leu : Ala : Trp : Glu G 2635 Arg : Ala : Asn	2540 Asn Ser Ile Leu Val 2620 Cys Val Arg Lys Ile 2700	Ala Leu Pro Cys 2605 Tyr Ala Leu Arg Thr 2685 Ser	Glu Trp Ser 2590 Asp Asn Phe Leu Ser 2670 Leu Glu	Thr 2575 Asn Thr His Pro Gln 2655 Ala Val	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu Ile Leu Ser
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As  Lys Tyr Arg Ty 26  Lys Lys Ile Me 2675  Cys Val Ser As 2690  Ser Asn Lys Tr	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu TO Lys Leu To Lys 263 In Arg Cys 2645 Ir Asp Thr 60 It Glu Arg Ile Ile Ir Ser Ser	2535 Lys Ilo O Tyr Pho Asp Gl Glu Pho 26 Ile Se 2615 Leu Al O Leu Se Glu Il Asp As 26 Ser Le 2695 Ala As	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro e Asp 2665 p Thr 80 u Ser	Lys 2570 Trp Arg Ile Met Glu 2650 Arg Ala Ala	Lys A 2555 Glu S Leu : Ala : Trp : Glu G 2635 Arg : Ala : Asn	2540 Asn Ser Ile Leu Val 2620 Cys Val Arg Lys Ile 2700 Val	Ala Leu Pro Cys 2605 Tyr Ala Leu Arg Thr 2685 Ser	Glu Trp Ser 2590 Asp Asn Phe Leu Ser 2670 Leu Glu	Thr 2575 Asn Thr His Pro Gln 2655 Ala Val	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu Ile Leu Ser
2530  Val Ser Lys Hi 2545  Gln Phe His Th  Lys Gly Ile Gl 25  Gly Lys Ala Gl 2595  Gly Val Asp Pr 2610  Arg Trp Ile Il 2625  Glu Phe Ala As  Lys Tyr Arg Ty 26  Lys Lys Ile Me 2675  Cys Val Ser As 2690	s Cys Ile 255 Ir Glu Asp 2565 In Leu Ala 80 Iy Lys Glu To Lys Leu 10 Lys Leu 10 Lys Leu 11 Lys 263 In Arg Cys 2645 Ir Asp Thr 860 It Glu Arg 11 Le 11 Ser Ser 271 14 Trp Tyr 2725	2535 Lys Ile  Tyr Phene Asp Glu Phene 26 Ile Se 2615 Leu Ale  Glu Il  Asp Ase 26 Ser Le 2695 Ala As  Ala Va	e Asn e Gly y Gly 2585 e Tyr 00 r Arg a Ala r Pro e Asp 2665 p Thr 80 u Ser p Thr	Ser Lys 2570 Trp Arg Ile Met Glu 2650 Arg Ala Ala Gln Ala 2730	Lys A 2555 Glu S Leu : Ala : Trp : Glu G 2635 Arg : Ala : Asn : Lys : 2715 Gln :	2540 Asn Ser Ile Leu Val 2620 Cys Val Arg Lys Ile 2700 Val Leu	Ala Leu Pro Cys 2605 Tyr Ala Leu Arg Thr 2685 Ser Ala Asp	Glu Trp Ser 2590 Asp Asn Phe Leu Ser 2670 Leu Glu Ile Pro	Thr 2575 Asn Thr His Pro 2655 Ala Thr Ile Pro 2735	Phe 2560 Gly Asp Pro Tyr Lys 2640 Leu Ser Glu 2720 Leu 5

```
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
       2755
                         2760
                                           2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
                                        2780
                     2775
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
                 2790
                                   2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
                                2810
              2805
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
          2820
                            2825
                                   2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu
                         2840
       2835
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
                     2855
                                       2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                  2870
                                    2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
             2885
                               2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
         2900
                2905
                                              2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
      2915
                        2920
                                           2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                     2935
                                       2940
Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln
                  2950
                                    2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
              2965
                                2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
          2980
                            2985
                                               2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
                        3000
                                           3005
       2995
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                     3015
                                       3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                 3030
                                    3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
                               3050
              3045
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
                             3065
          3060
                                               3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
                                           3085
       3075
                         3080
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
                                       3100
                     3095
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
                                    3115
                 3110
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
                                3130
              3125
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
                            3145
                                              3150
          3140
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
                              3165
                         3160
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
                                        3180
                     3175
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
                  3190
                                    3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
```

3205 3210 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu 3220 3225 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met 3240 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn 3255 3260 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro 3270 3275 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys 3285 3290 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile 3300 3305 3310 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe 3315 3320 3325 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu 3335 3340 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys 3350 3355 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser 3365 3370 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys 3380 3385 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys 3400 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile 3410 3415

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: other

TGAGTTTTAC CTCAGTCACA

- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C	41
(2) INFORMATION FOR SEQ ID NO:16:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 24 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
GATCTTTAAC TGTTCTGGGT CACA	24
(2) INFORMATION FOR SEQ ID NO:17:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE  (A) NAME/KEY: other  (B) LOCATION: 122  (D) OTHER INFORMATION: 3RII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
CCCAGCATGA CACAATTAAT GA	22
(2) INFORMATION FOR SEQ ID NO:18:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 44 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 144</pre>	

(D) OTHER INFORMATION: 4F/M 13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA	44
(2) INFORMATION FOR SEQ ID NO:19:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 4R-1A primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
ATCAGATTCA TCTTTATAGA AC	22
(2) INFORMATION FOR SEQ ID NO:20:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE     (A) NAME/KEY: other     (B) LOCATION: 140     (D) OTHER INFORMATION: 5+6F/M13F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA	40
(2) INFORMATION FOR SEQ ID NO:21:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 38 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	

<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 138   (D) OTHER INFORMATION: 5+6R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT	38
(2) INFORMATION FOR SEQ ID NO:22:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 138</li><li>(D) OTHER INFORMATION: 7F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA	38
(2) INFORMATION FOR SEQ ID NO:23:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 36 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 136   (D) OTHER INFORMATION: 7R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC	36
(2) INFORMATION FOR SEQ ID NO:24:	

(ii) MOLECULE TYPE: Genomic DNA

(A) LENGTH: 40 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other</pre>	
(B) LOCATION: 140	
(D) OTHER INFORMATION: 8F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA	40
(2) INFORMATION FOR SEQ ID NO:25:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li></ul>	
(B) TYPE: nucleic acid	
<ul><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ix) FEATURE:	
(A) NAME/KEY: other	
(B) LOCATION: 122 (D) OTHER INFORMATION: 8FIA primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
TTGCATTCTA GTGATAATAT AC	22
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 19 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(D) TOPOLOGI: Tilleat	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other</pre>	
(B) LOCATION: 119	
(D) OTHER INFORMATION: 8RIA primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	

(i) SEQUENCE CHARACTERISTICS:

19 AATTGTTAGC AATTTCAAC (2) INFORMATION FOR SEQ ID NO:27: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 1...40 (D) OTHER INFORMATION: 9F/M13F primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: 40 TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT (2) INFORMATION FOR SEQ ID NO:28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9R/M13R primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

### CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs(B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
  - (ix) FEATURE
    - (A) NAME/KEY: other

(D) OTHER INFORMATION: 10AF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GAATAATATA AATTATATGG CTTA	24
(2) INFORMATION FOR SEQ ID NO:30:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 137</li><li>(D) OTHER INFORMATION: 10AR/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT	37
(2) INFORMATION FOR SEQ ID NO:31:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 42 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 142</li><li>(D) OTHER INFORMATION: 10BF/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
TGTAAAACGA CGGCCAGTAR CTGAAGTGGA ACCAAATGAT AC	42
(2) INFORMATION FOR SEQ ID NO:32:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 44 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(B) LOCATION: 1...24

(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 144</li><li>(D) OTHER INFORMATION: 10BR/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA	44
(2) INFORMATION FOR SEQ ID NO:33:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE:	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 10CF/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG	40
(2) INFORMATION FOR SEQ ID NO:34:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 19 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	•
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 119   (D) OTHER INFORMATION: 10CRII primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AGACAGAGGT ACCTGAATC	19

(ii) MOLECULE TYPE: Genomic DNA

(2) INFORMATION FOR SEQ ID NO:35:

<ul><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 140 (D) OTHER INFORMATION: 11AF-M13 primer	
(b) dillik intoknittok. Tim mis primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACTT	40
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS:	
<ul><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 137 (D) OTHER INFORMATION: 11AR-M13 primer	
•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT	37
(2) INFORMATION FOR SEQ ID NO:37:	
(i) SEQUENCE CHARACTERISTICS:	
<ul><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 122 (D) OTHER INFORMATION: 11BF primer	

(i) SEQUENCE CHARACTERISTICS:

AAGAAGCAAA ATGTAATAAG GA	22
(2) INFORMATION FOR SEQ ID NO:38:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11BR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CATTTAAAGC ACATACATCT TG	22
(2) INFORMATION FOR SEQ ID NO:39:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: primer   (B) LOCATION:   (D) OTHER INFORMATION: 11CF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
TCTAGAGGCA AAGAATCATA C	21
(2) INFORMATION FOR SEQ ID NO:40:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11CR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CAAGATTATT CCTTTCATTA GC	22
(2) INFORMATION FOR SEQ ID NO:41:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 11DF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
AACCAAAACA CAAATCTAAG AG	22
(2) INFORMATION FOR SEQ ID NO:42:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 23 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 123   (D) OTHER INFORMATION: 11DR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GTCATTTTTA TATGCTGCTT TAC	23
(2) INFORMATION FOR SEQ ID NO:43:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li></ul>	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 11EF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
GGTTTTATAT GGAGACACAG G	21
(2) INFORMATION FOR SEQ ID NO:44:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 123   (D) OTHER INFORMATION: 11ER primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
GTATTTACAA TTTCAACACA AGC	23
(2) INFORMATION FOR SEQ ID NO:45:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 11FF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	

(B) TYPE: nucleic acid

ATCACAGTTT TGGAGGTAGC	20
(2) INFORMATION FOR SEQ ID NO:46:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 121</li><li>(D) OTHER INFORMATION: 11FR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
CTGACTTCCT GATTCTTCTA A	21
(2) INFORMATION FOR SEQ ID NO:47:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11GF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
CTCAGATGTT ATTTTCCAAG C	21
(2) INFORMATION FOR SEQ ID NO:48:	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(D) OTHER INFORMATION: 11GR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
CTGTTAAATA ACCAGAAGCA C	21
(2) INFORMATION FOR SEQ ID NO:49:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 18 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 118   (D) OTHER INFORMATION: 11HF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
AGGTAGACAG CAGCAAGC	18
(2) INFORMATION FOR SEQ ID NO:50:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ix) FEATURE:	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11HR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
GTAATATCAG TTGGCATTTA TT	22
(2) INFORMATION FOR SEQ ID NO:51:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

(B) LOCATION: 1...21

(B) LOCATION: 121 (D) OTHER INFORMATION: 11IF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
TGCAGAGGTA CATCCAATAA G	21
(2) INFORMATION FOR SEQ ID NO:52:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11IR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GATCAGTAAA TAGCAAGTCC G	21
(2) INFORMATION FOR SEQ ID NO:53:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 123   (D) OTHER INFORMATION: 11JF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
TACTGAAAAT GAAGATAACA AAT	23
(2) INFORMATION FOR SEQ ID NO:54:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

(A) NAME/KEY: other

(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
ATTTTGTTCT TTCTTATGTC AG	22
(2) INFORMATION FOR SEQ ID NO:55:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 135   (D) OTHER INFORMATION: 11KF-M13 primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA	35
(2) INFORMATION FOR SEQ ID NO:56:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 35 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 135</li><li>(D) OTHER INFORMATION: 11KR-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG	35
(2) INFORMATION FOR SEQ ID NO:57:	

(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 11LF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
CACAAAATAC TGAAAGAAAG TG	22
(2) INFORMATION FOR SEQ ID NO:58:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 19 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 119</li><li>(D) OTHER INFORMATION: 11LR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GGCACCACAG TCTCAATAG	19
(2) INFORMATION FOR SEQ ID NO:59:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 11MF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	

2	0

GCAAAGACCC TAAAGTACAG	20
(2) INFORMATION FOR SEQ ID NO:60:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11MR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
CATCAAATAT TCCTTCTCA AG	22
(2) INFORMATION FOR SEQ ID NO:61:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 135</li><li>(D) OTHER INFORMATION: 11NF-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC	35
(2) INFORMATION FOR SEQ ID NO:62:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 35 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

- (ii) MOLECULE TYPE: Genomic DNA
  - (ix) FEATURE

(B) LOCATION: 135 (D) OTHER INFORMATION: 11NR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT	35
(2) INFORMATION FOR SEQ ID NO:63:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 110F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GTACTATAGC TGAAAATGAC AA	22
(2) INFORMATION FOR SEQ ID NO:64:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 110R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
ACCACTGGCT ATCCTAAATG	20
(2) INFORMATION FOR SEQ ID NO:65:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

(A) NAME/KEY: other

(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 11PF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
TGAAGATATT TGCGTTGAGG	20
(2) INFORMATION FOR SEQ ID NO:66:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 11PR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
GTCAGCAAAA ACCTTATGTG	20
(2) INFORMATION FOR SEQ ID NO:67:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11QF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
ACGAAAATTA TGGCAGGTTG T	21

(D) TOPOLOGY: linear

<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11QR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
CTTGTCTTGC GTTTTGTAAT G	21
(2) INFORMATION FOR SEQ ID NO:69:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 11RF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
GCTTCATAAG TCAGTCTCAT	20
(2) INFORMATION FOR SEQ ID NO:70:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 11RR primer</li></ul>	

(2) INFORMATION FOR SEQ ID NO:68:

TCAAATTCCT CTAACACTCC	20
(2) INFORMATION FOR SEQ ID NO:71:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 135   (D) OTHER INFORMATION: 11SF-M13 primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC	35
(2) INFORMATION FOR SEQ ID NO:72:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 137   (D) OTHER INFORMATION: 11SR-M13 primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT	37
(2) INFORMATION FOR SEQ ID NO:73:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

(11) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 11TF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
GTTCTTCAGA AAATAATCAC TC	22
(2) INFORMATION FOR SEQ ID NO:74:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 11TR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
TGTAAAAAGA GAATGTGTGG C	21
(2) INFORMATION FOR SEQ ID NO:75:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 139</li><li>(D) OTHER INFORMATION: 11UF-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
TGTAAAACGA CGGCCAGTAC TTTTTCTGAT GTTCCTGTG	39

(2) INFORMATION FOR SEQ ID NO:76:

<ul><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 139</li><li>(D) OTHER INFORMATION: 11UR-M13 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA	39
(2) INFORMATION FOR SEQ ID NO:77:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 42 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 142</li><li>(D) OTHER INFORMATION: 12F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA	42
(2) INFORMATION FOR SEQ ID NO:78:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 140   (D) OTHER INFORMATION: 12R/M13R primer</pre>	

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA	40
(2) INFORMATION FOR SEQ ID NO:79:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 13-2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
TAACATTTAA GCATCCGTTA C	21
(2) INFORMATION FOR SEQ ID NO:80:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 28 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 128   (D) OTHER INFORMATION: 13-2R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
AAACGAGACT TTTCTCATAC TGTATTAG	28
(2) INFORMATION FOR SEQ ID NO:81:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	

(ii) MOLECULE TYPE: Genomic DNA

<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 122</li><li>(D) OTHER INFORMATION: 14F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
ACCATGTAGC AAATGAGGGT CT	22
(2) INFORMATION FOR SEQ ID NO:82:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 122   (D) OTHER INFORMATION: 14AR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GCTTTTGTCT GTTTTCCTCC AA	22
(2) INFORMATION FOR SEQ ID NO:83:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 121   (D) OTHER INFORMATION: 15-2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
CCAGGGGTTG TGCTTTTAA A	21
(2) INFORMATION FOR SEQ ID NO:84:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li></ul>	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: primer   (B) LOCATION:   (D) OTHER INFORMATION: 15FUT/M13-R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC	38
(2) INFORMATION FOR SEQ ID NO:85:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 124</li><li>(D) OTHER INFORMATION: 16AF primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TTTGGTTTGT TATAATTGTT TTTA	24
(2) INFORMATION FOR SEQ ID NO:86:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 16AR primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single

CCAACTTTT AGTTCGAGAG 20

(2) INFORMATION FOR SEQ ID NO:87:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 19 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 119   (D) OTHER INFORMATION: 17F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
TTCAGTATCA TCCTATGTG	19
(2) INFORMATION FOR SEQ ID NO:88:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 17AR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
AGAAACCTTA ACCCATACTG	20
(2) INFORMATION FOR SEQ ID NO:89:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other</pre>	

(B) LOCATION: 139 (D) OTHER INFORMATION: 18FUT/M13-AF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC	3 9
(2) INFORMATION FOR SEQ ID NO:90:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 138   (D) OTHER INFORMATION: 18R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG	38
(2) INFORMATION FOR SEQ ID NO:91:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 41 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 141   (D) OTHER INFORMATION: 19F/M13F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T	41
(2) INFORMATION FOR SEQ ID NO:92:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC	39
(2) INFORMATION FOR SEQ ID NO:93:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 138</li><li>(D) OTHER INFORMATION: 20F/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC	38
(2) INFORMATION FOR SEQ ID NO:94:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 139</li><li>(D) OTHER INFORMATION: 20R/M13R primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA	39

(2) INFORMATION FOR SEQ ID NO:95:

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(D) TOPOLOGI: TIMEAL	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other	
(B) LOCATION: 139	
(D) OTHER INFORMATION: 21F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT	39
IGIAAAACGA CGGCCAGIGG GIGIIIIAIG CIIGGIICI	39
(2) INFORMATION FOR SEQ ID NO:96:	
(-)	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
•	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 140	
(D) OTHER INFORMATION: 21R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG	40
(2) INDODMETON FOR GEO ID NO.07.	
(2) INFORMATION FOR SEQ ID NO:97:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 19 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(II) MODECORE IIPE: GENOMIC DIM	
(ix) FEATURE	
(ix) FEATURE	
<pre>(ix) FEATURE  (A) NAME/KEY: other (B) LOCATION: 119</pre>	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs

(D) OTHER INFORMATION: 22F-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
AACCACACCC TTAAGATGA	19
(2) INFORMATION FOR SEQ ID NO:98:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 22R-1A primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
GCATTAGTAG TGGATTTTGC	20
(2) INFORMATION FOR SEQ ID NO:99:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 16 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 116</li><li>(D) OTHER INFORMATION: 23FII primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
TCACTTCCAT TGCATC	16
(2) INFORMATION FOR SEQ ID NO:100:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 17 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 117   (D) OTHER INFORMATION: 23RII primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
TGCCAACTGG TAGCTCC	17
(2) INFORMATION FOR SEQ ID NO:101:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 24 2F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
TACAGTTAGC AGCGACAAAA	20
(2) INFORMATION FOR SEQ ID NO:102:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 38 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other     (B) LOCATION: 138     (D) OTHER INFORMATION: 24R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC	38

(2) INFORMATION FOR SEQ ID NO:103:

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 25F-7/23 primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
GCTTTCGCCA AATTCAGCTA	20
(2) INFORMATION FOR SEQ ID NO:104:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
<ul><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 120</li><li>(D) OTHER INFORMATION: 25R-7/23 primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
TACCAAAATG TGTGGTGATG	20
(2) INFORMATION FOR SEQ ID NO:105:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 120   (D) OTHER INFORMATION: 26-2F primer</pre>	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs

AATCACTGAT ACTGGTTTTG	20
(2) INFORMATION FOR SEQ ID NO:106:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other     (B) LOCATION: 120     (D) OTHER INFORMATION: 26-2R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
TATACTTACA GGAGCCACAT	20
(2) INFORMATION FOR SEQ ID NO:107:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 118   (D) OTHER INFORMATION: 27AF-1A primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
CTGTGTGTAA TATTTGCG	18
(2) INFORMATION FOR SEQ ID NO:108:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other    (B) LOCATION: 140    (D) OTHER INFORMATION: 27AR/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG	40
(2) INFORMATION FOR SEQ ID NO:109:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<ul><li>(ix) FEATURE</li><li>(A) NAME/KEY: other</li><li>(B) LOCATION: 140</li><li>(D) OTHER INFORMATION: 27BF/M13F primer</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA	40
(2) INFORMATION FOR SEQ ID NO:110:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE   (A) NAME/KEY: other   (B) LOCATION: 138   (D) OTHER INFORMATION: 27BR/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:	
CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA	38

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1158 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1...1158
  - (D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence
- (ix) FEATURE
  - (A) NAME/KEY: variable
  - (B) LOCATION: 102...602
  - (D) OTHER INFORMATION: M at positions 102 or 351 = A or C; R at position 602 = A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60 AAGTAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120 TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180 GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240 AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTTG 300 TATCTGAAGT GGAACCAAAT GATACTGATC CATTAGATTC AAATGTAGCA MATCAGAAGC 360 CCTTTGAGAG TGGAAGTGAC AAAATCTCCA AGGAAGTTGT ACCGTCTTTG GCCTGTGAAT 420 GGTCTCAACT AACCCTTTCA GGTCTAAATG GAGCCCAGAT GGAGAAAATA CCCCTATTGC 480 ATATTTCTTC ATGTGACCAA AATATTTCAG AAAAAGACCT ATTAGACACA GAGAACAAAA 540 GAAAGAAAGA TTTTCTTACT TCAGAGAATT CTTTGCCACG TATTTCTAGC CTACCAAAAT 600 CRGAGAAGCC ATTAAATGAG GAAACAGTGG TAAATAAGAG AGATGAAGAG CAGCATCTTG 660 AATCTCATAC AGACTGCATT CTTGCAGTAA AGCAGGCAAT ATCTGGAACT TCTCCAGTGG 720 CTTCTTCATT TCAGGGTATC AAAAAGTCTA TATTCAGAAT AAGAGAATCA CCTAAAGAGA 780 CTTTCAATGC AAGTTTTTCA GGTCATATGA CTGATCCAAA CTTTAAAAAA GAAACTGAAG 840 CCTCTGAAAG TGGACTGGAA ATACATACTG TTTGCTCACA GAAGGAGGAC TCCTTATGTC 900 CAAATTTAAT TGATAATGGA AGCTGGCCAG CCACCACCAC ACAGAATTCT GTAGCTTTGA 960 AGAATGCAGG TTTAATATCC ACTTTGAAAA AGAAAACAAA TAAGTTTATT TATGCTATAC 1020 ATGATGAAAC ATTTTATAAA GGAAAAAAA TACCGAAAGA CCAAAAATCA GAACTAATTA 1080 ACTGTTCAGC CCAGTTTGAA GCAAATGCTT TTGAAGCACC ACTTACATTT GCAAATGCTG 1140 ATTCAGGTAC CTCTGTCT 1158

- (2) INFORMATION FOR SEQ ID NO:112:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4987 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1...4987
  - (D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence

### (ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 339...1917
- (D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T; R at positions 790, 1081 or 1506 = A or G.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTTGTGTTTT TATGTTTAGG TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60 GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAATTCT GAGGAAATGT 120 TCTAGAAATG AAACATGTTC TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180 GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240 TGCCTGCAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300 GAAGAGGTCT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360 ACTGACTTC AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420 TTAACTCCTA CTTCCAAGGA TGTTCTGTCA AACCTAGTCA TGATTTCTAG AGGCAAAGAA 480 TCATACAAAA TGTCAGACAA GCTCAAAGGT AACAATTATG AATCTGATGT TGAATTAACC 540 AAAAATATTC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAAAC 600 GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660 TTCAACCAAA ACACAAATCT AAGAGTAATC CAAAAAAATC AAGAAGAAAC TACTTCAATT 720 TCAAAAATAA CTGTCAATCC AGACTCTGAA GAACTTTTCT CAGACAATGA GAATAATTTT 780 GTCTTCCAAR TAGCTAATGA AAGGAATAAT CTTGCTTTAG GAAATACTAA GGAACTTCAT 840 GAAACAGACT TGACTTGTGT AAACGAACCC ATTTTCAAGA ACTCTACCAT GGTTTTATAT 900 GGAGACACAG GTGATAAACA AGCAACCCAA GTGTCAATTA AAAAAGATTT GGTTTATGTT 960 CTTGCAGAGG AGAACAAAA TAGTGTAAAG CAGCATATAA AAATGACTCT AGGTCAAGAT 1020 TTAAAATCGG ACATCTCCTT GAATATAGAT AAAATACCAG AAAAAAATAA TGATTACATG 1080 RACAAATGGG CAGGACTCTT AGGTCCAATT TCAAATCACA GTTTTGGAGG TAGCTTCAGA 1140 ACAGCTTCAA ATAAGGAAAT CAAGCTCTCT GAACATAACA TTAAGAAGAG CAAAATGTTC 1200 TTCAAAGATA TTGAAGAACA ATATCCTACT AGTTTAGCTT GTGTTGAAAT TGTAAATACC 1260 TTGGCATTAG ATAATCAAAA GAAACTGAGC AAGCCTCAGT CAATTAATAC TGTATCTGCA 1320 CATTTACAGA GTAGTGTAGT TGTTTCTGAT TGTAAAAATA GTCATATAAC CCCTCAGATG 1380 TTATTTCCA AGCAGGATTT TAATTCAAAC CATAATTTAA CACCTAGCCA AAAGGCAGAA 1440 ATTACAGAAC TTTCTACTAT ATTAGAAGAA TCAGGAAGTC AGTTTGAATT TACTCAGTTT 1500 AGAAARCCAA GCTACATATT GCAGAAGAGT ACATTTGAAG TGCCTGAAAA CCAGATGACT 1560 ATCTTAAAGA CCACTTCTGA GGAATGCAGA GATGCTGATC TTCATGTCAT AATGAATGCC 1620 CCATCGATTG GTCAGGTAGA CAGCAGCAAG CAATTTGAAG GTACAGTTGA AATTAAACGG 1680 AAGTTTGCTG GCCTGTTGAA AAATGACTGT AACAAAAGTG CTTCTGGTTA TTTAACAGAT 1740 GAAAATGAAG TGGGGTTTAG GGGCTTTTAT TCTGCTCATG GCACAAAACT GAATGTTTCT 1800 ACTGAAGCTC TGCAAAAAGC TGTGAAACTG TTTAGTGATA TTGAGAATAT TAGTGAGGAA 1860 ACTTCTGCAG AGGTACATCC AATAAGTTTA TCTTCAAGTA AATGTCATGA TTCTGTYGTT 1920 TCAATGTTTA AGATAGAAAA TCATAATGAT AAAACTGTAA GTGAAAAAAA TAATAAATGC 1980 CAACTGATAT TACAAAATAA TATTGAAATG ACTACTGGCA CTTTTGTTGA AGAAATTACT 2040 GAAAATTACA AGAGAAATAC TGAAAATGAA GATAACAAAT ATACTGCTGC CAGTAGAAAT 2100 TCTCATAACT TAGAATTTGA TGGCAGTGAT TCAAGTAAAA ATGATACTGT TTGTATTCAT 2160 AAAGATGAAA CGGACTTGCT ATTTACTGAT CAGCACAACA TATGTCTTAA ATTATCTGGC 2220 CAGTTTATGA AGGAGGGAAA CACTCAGATT AAAGAAGATT TGTCAGATTT AACTTTTTTG 2280 GAAGTTGCGA AAGCTCAAGA AGCATGTCAT GGTAATACTT CAAATAAAGA ACAGTTAACT 2340 GCTACTAAAA CGGAGCAAAA TATAAAAGAT TTTGAGACTT CTGATACATT TTTTCAGACT 2400 GCAAGTGGGA AAAATATTAG TGTCGCCAAA GAGTCATTTA ATAAAATTGT AAATTTCTTT 2460 GATCAGAAAC CAGAAGAATT GCATAACTTT TCCTTAAATT CTGAATTACA TTCTGACATA 2520 AGAAAGAACA AAATGGACAT TCTAAGTTAT GAGGAAACAG ACATAGTTAA ACACAAAATA 2580 CTGAAAGAAA GTGTCCCAGT TGGTACTGGA AATCAACTAG TGACCTTCCA GGGACAACCC 2640 GAACGTGATG AAAAGATCAA AGAACCTACT CTGTTGGGTT TTCATACAGC TAGCGGGAAA 2700 AAAGTTAAAA TTGCAAAGGA ATCTTTGGAC AAAGTGAAAA ACCTTTTTGA TGAAAAAGAG 2760 CAAGGTACTA GTGAAATCAC CAGTTTTAGC CATCAATGGG CAAAGACCCT AAAGTACAGA 2820 GAGGCCTGTA AAGACCTTGA ATTAGCATGT GAGACCATTG AGATCACAGC TGCCCCAAAG 2880

```
TGTAAAGAAA TGCAGAATTC TCTCAATAAT GATAAAAACC TTGTTTCTAT TGAGACTGTG 2940
GTGCCACCTA AGCTCTTAAG TGATAATTTA TGTAGACAAA CTGAAAATCT CAAAACATCA 3000
AAAAGTATCT TTTTGAAAGT TAAAGTACAT GAAAATGTAG AAAAAGAAAC AGCAAAAAGT 3060
CCTGCAACTT GTTACACAAA TCAGTCCCCT TATTCAGTCA TTGAAAATTC AGCCTTAGCT 3120
TTTTACACAA GTTGTAGTAG AAAAACTTCT GTGAGTCAGA CTTCATTACT TGAAGCAAAA 3180
AAATGGCTTA GAGAAGGAAT ATTTGATGGT CAACCAGAAA GAATAAATAC TGCAGATTAT 3240
GTAGGAAATT ATTTGTATGA AAATAATTCA AACAGTACTA TAGCTGAAAA TGACAAAAAT 3300
CATCTCTCCG AAAAACAAGA TACTTATTTA AGTAACAGTA GCATGTCTAA CAGCTATTCC 3360
TACCATTCTG ATGAGGTATA TAATGATTCA GGATATCTCT CAAAAAATAA ACTTGATTCT 3420
GGTATTGAGC CAGTATTGAA GAATGTTGAA GATCAAAAAA ACACTAGTTT TTCCAAAGTA 3480
ATATCCAATG TAAAAGATGC AAATGCATAC CCACAAACTG TAAATGAAGA TATTTGCGTT 3540
GAGGAACTTG TGACTAGCTC TTCACCCTGC AAAAATAAAA ATGCAGCCAT TAAATTGTCC 3600
ATATCTAATA GTAATAATTT TGAGGTAGGG CCACCTGCAT TTAGGATAGC CAGTGGTAAA 3660
ATCGTTTGTG TTTCACATGA AACAATTAAA AAAGTGAAAG ACATATTTAC AGACAGTTTC 3720
AGTAAAGTAA TTAAGGAAAA CAACGAGAAT AAATCAAAAA TTTGCCAAAC GAAAATTATG 3780
GCAGGTTGTT ACGAGGCATT GGATGATTCA GAGGATATTC TTCATAACTC TCTAGATAAT 3840
GATGAATGTA GCACGCATTC ACATAAGGTT TTTGCTGACA TTCAGAGTGA AGAAATTTTA 3900
CAACATAACC AAAATATGTC TGGATTGGAG AAAGTTTCTA AAATATCACC TTGTGATGTT 3960
AGTTTGGAAA CTTCAGATAT ATGTAAATGT AGTATAGGGA AGCTTCATAA GTCAGTCTCA 4020
TCTGCAAATA CTTGTGGGAT TTTTAGCACA GCAAGTGGAA AATCTGTCCA GGTATCAGAT 4080
GCTTCATTAC AAAACGCAAG ACAAGTGTTT TCTGAAATAG AAGATAGTAC CAAGCAAGTC 4140
TTTTCCAAAG TATTGTTTAA AAGTAACGAA CATTCAGACC AGCTCACAAG AGAAGAAAAT 4200
ACTGCTATAC GTACTCCAGA ACATTTAATA TCCCAAAAAG GCTTTTCATA TAATGTGGTA 4260
AATTCATCTG CTTTCTCTGG ATTTAGTACA GCAAGTGGAA AGCAAGTTTC CATTTTAGAA 4320
AGTTCCTTAC ACAAAGTTAA GGGAGTGTTA GAGGAATTTG ATTTAATCAG AACTGAGCAT 4380
AGTCTTCACT ATTCACCTAC GTCTAGACAA AATGTATCAA AAATACTTCC TCGTGTTGAT 4440
AAGAGAAACC CAGAGCACTG TGTAAACTCA GAAATGGAAA AAACCTGCAG TAAAGAATTT 4500
AAATTATCAA ATAACTTAAA TGTTGAAGGT GGTTCTTCAG AAAATAATCA CTCTATTAAA 4560
GTTTCTCCAT ATCTCTCTA ATTTCAACAA GACAAACAAC AGTTGGTATT AGGAACCAAA 4620
GTCTCACTTG TTGAGAACAT TCATGTTTTG GGAAAAGAAC AGGCTTCACC TAAAAACGTA 4680
AAAATGGAAA TTGGTAAAAC TGAAACTTTT TCTGATGTTC CTGTGAAAAC AAATATAGAA 4740
GTTTGTTCTA CTTACTCCAA AGATTCAGAA AACTACTTTG AAACAGAAGC AGTAGAAATT 4800
GCTAAAGCTT TTATGGAAGA TGATGAACTG ACAGATTCTA AACTGCCAAG TCATGCCACA 4860
CATTCTCTTT TTACATGTCC CGAAAATGAG GAAATGGTTT TGTCAAATTC AAGAATTGGA 4920
AAAAGAAGAG GAGAGCCCCT TATCTTAGTG GGTAAGTGTT CATTTTTACC TTTCGTGTTG 4980
                                                                   4987
CCAATCA
```

### (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 468 base pairs
  - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1...468
  - (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence
- (ix) FEATURE
  - (A) NAME/KEY: variable
  - (B) LOCATION: 248
  - (D) OTHER INFORMATION: R at position 248 = A or G.

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
- CCCCATTGCA GCACAACTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
  GGTCAAGAAT TTCTGTCTAA ATCTCATTTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
  AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
  ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCCACC TTTTAAAACT 240
  AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAACTTGGA GGAAAACAGA 300
  CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAT 360
  GAGATTCATC AGTTTAACAA AAACAACTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
  TGTGGAAGAG AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT TACCAAAG 420
  - (2) INFORMATION FOR SEQ ID NO:114:
  - (i) SEOUENCE CHARACTERISTICS:
    - (A) LENGTH: 255 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (ix) FEATURE
    - (A) NAME/KEY: exon
    - (B) LOCATION: 1...255
    - (D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence
  - (ix) FEATURE
    - (A) NAME/KEY: variable
    - (B) LOCATION: 127
    - (D) OTHER INFORMATION: R at position 127 = A or G.
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTTTTATTCC AATATCTTAA ATGGTCACAG GGTTATTCA GTGAAGAGCA GTTAAGAGCC 60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT 120
AGGAAGRCCA TGGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTCACAACC 180
GTGTGGAAGT TGCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA 240
AATGCTTTGT TTTTA

- (2) INFORMATION FOR SEQ ID NO:115:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 31...135
  - (D) OTHER INFORMATION: Exon 2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TAAGTGCATT TTGGTCTTCT GTTTTGCAGA CTTATTTACC AAGCATTGGA GGAATATCGT 60 AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC 120

- (2) INFORMATION FOR SEQ ID NO:116:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 21...269
  - (D) OTHER INFORMATION: Exon 3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGGATTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTT AAGAACTTTC 60
TTCAGAAGCT CCACCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACTCCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180
AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297

- (2) INFORMATION FOR SEQ ID NO:117:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 159 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 26...134
  - (D) OTHER INFORMATION: Exon 4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TCACTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60 CGCACAGTGA AAACTAAAAT GGATCAAGCA GATGATGTT CCTGTCCACT TCTAAATTCT 120 TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159

- (2) INFORMATION FOR SEQ ID NO:118:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 31...71
  - (D) OTHER INFORMATION: Exon 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
TTAACAATTT TCCCCTTTTT TTACCCCCAG TGGTATGTGG GAGTTTGTTT CATACACCAA 60 80
(2) INFORMATION FOR SEQ ID NO:119:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 174 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>
<ul> <li>(ii) MOLECULE TYPE: Genomic DNA</li> <li>(ix) FEATURE</li> <li>(A) NAME/KEY: exon</li> <li>(B) LOCATION: 51165</li> <li>(D) OTHER INFORMATION: Exon 7</li> </ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
TAATGATCAG GGCATTTCTA TAAAAAATAA ACTATTTCT TTCCTCCAG GGTCGTCAGA 60 CACCAAAACA TATTTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 12 GTTCTTTAGC TACACCACCC ACCCTTAGTT CTACTGTGCT CATAGGTAAT AATA 17
(2) INFORMATION FOR SEQ ID NO:120:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 90 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>
<ul> <li>(ii) MOLECULE TYPE: Genomic DNA</li> <li>(ix) FEATURE</li> <li>(A) NAME/KEY: exon</li> <li>(B) LOCATION: 1463</li> <li>(D) OTHER INFORMATION: Exon 8</li> </ul>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTTCCTCA TGATACTACT 60

- (2) INFORMATION FOR SEQ ID NO:121:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 142 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

GCTGTAAGTA AATATGACAT TGATTAGACT

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 20...131

- (D) OTHER INFORMATION: Exon 9

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

  TAAACTATAA TTTTTGCAGA ATGTGAAAAG CTATTTTTCC AATCATGATG AAAGTCTGAA 60
  GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120
- TGCAAGTCAT GGTAAGTCCT CT

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 29...124
  - (D) OTHER INFORMATION: Exon 12
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60 GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120 GATGGTAAAA TTAGCTTTTT ATTTATA 147

- (2) INFORMATION FOR SEQ ID NO:123:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 125 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 31...100
  - (D) OTHER INFORMATION: Exon 13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60 ATCATGTTC TTTAGAGCCG ATTACCTGTG TACCCTTTCG GTAAGACATG TTTAAAATTTT 120 TCTAA

- (2) INFORMATION FOR SEQ ID NO:124:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 199 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
  (ix) FEATURE
  - (A) NAME/KEY: exon(B) LOCATION: 13...183
  - (D) OTHER INFORMATION: Exon 17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TTATTTGTTC AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTAT AATCACTATA GATGGATCAT ATGGAAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT 199

- (2) INFORMATION FOR SEQ ID NO:125:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 19...373
  - (D) OTHER INFORMATION: Exon 18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

TTTTGTTTC ACTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60
AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACACTT GTTCTCTGTG TTTCTGACAT 120
AATTTCATTG AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180
CCAAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240
TCCTCCCCTC TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300
TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360
TCTTATGTTA AAGGTAAATT

- (2) INFORMATION FOR SEQ ID NO:126:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 30...185
  - (D) OTHER INFORMATION: Exon 19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60 GGTATACCAA ACTTGGATTC TTTCCTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120 TTTTCAGTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180 TACAGGTATG ATGTATTCTT GAAACTTA 208

- (2) INFORMATION FOR SEQ ID NO:127:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 28...172
  - (D) OTHER INFORMATION: Exon 20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
TTTCGCAATG AAAGAGAGA AGAAAAGGAA GCAGCAAAAAT ATGTGGAGGC CCAACAAAAG 120
AGACTAGAAG CCTTATTCAC TAAAATTCAG GAGGAATTTG AAGAACATGA AGGTAAAATT 180
AGTTATATGG TACACATTGT TATTTC 206

- (2) INFORMATION FOR SEQ ID NO:128:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 185 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 36...157
  - (D) OTHER INFORMATION: Exon 21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGTTTAGTGA ATTAATAATC CTTTTGTTTT CTTAGAAAAC ACAACAAAAC CATATTTACC 60 ATCACGTGCA CTAACAAGAC AGCAAGTTCG TGCTTTGCAA GATGGTGCAG AGCTTATGA 120 AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180 ATGAG

- (2) INFORMATION FOR SEQ ID NO:129:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 12...175
  - (D) OTHER INFORMATION: Exon 23

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
AGAAGGAAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAAACTCAG TATCAACAAC TACCGGTACA 180
AACCTTTCAT TGTAATTTTT 200

- (2) INFORMATION FOR SEQ ID NO:130:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 217 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 25...163
  - (D) OTHER INFORMATION: Exon 24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTTTTGT TTTGTTTTCT GTAGGTTTCA GATGAAATTT TATTTCAGAT TTACCAGCCA 60
CGGGAGCCCC TTCACTTCAG CAAATTTTTA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
GTGGACCTAA TAGGATTTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
TAATTTTTTT TATTGATTCT TTTAAAAAAAC ATTGTCT 217

- (2) INFORMATION FOR SEQ ID NO:131:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 284 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 31...275
  - (D) OTHER INFORMATION: Exon 25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TAACATTCTT TTCTTTTTT TCCATTCTAG GACTTGCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA 284

- (2) INFORMATION FOR SEQ ID NO:132:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 31...177
  - (D) OTHER INFORMATION: Exon 26
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ATAAAGCAGC TTTTCCACTT ATTTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60 AACAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCCC AACTAAAGAC 120 TGTACTTCAG GGCCGTACAC TGCTCAAATC ATTCCTGGTA CAGGAAACAA GCTTCTGGTA 180 AGTTAATGTA AACTCAAGGA ATATTATAAG 210

- (2) INFORMATION FOR SEQ ID NO:133:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 691 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
  - (A) NAME/KEY: exon
  - (B) LOCATION: 23...691
  - (D) OTHER INFORMATION: Exon 27
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TACGTTTTCA TTTTTTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60
TTTATCACTT TGTATGGCCA AAAGGAAGTC TGTTTCCACA CCTGTCTCAG CCCAGATGAC 120
TTCAAAGTCT TGTAAAGGGG AGAAAGAGAT TGATGACCAA AAGAACTGCA AAAAGAGAAG 180
AGCCTTGGAT TTCTTGAGTA GACTGCCTTT ACCTCCACCT GTTAGTCCCA TTTGTACATT 240
TGTTTCTCCG GCTGCACAGA AGGCATTTCA GCCACCAAGG AGTTGTGGCA CCAAATACGA 300
AACACCCATA AAGAAAAAAG AACTGAATTC TCCTCAGATG ACTCCATTTA AAAAATTCAA 360
TGAAATTTCT CTTTTGGAAA GTAATTCAAT AGCTGACGAA GAACTTGCAT TGATAAATAC 420
CCAAGCTCTT TTGTCTGGTT CAACAGGAGA AAAACAATTT ATATCTGTCA GTGAATCCAC 480
TAGGACTGCT CCCACCAGTT CAGAAGATTA TCTCAGACTG AAACGACGTT GTACTACATC 540
TCTGATCAAA GAACAGGAGA GTTCCCAGGC CAGTACGGAA GAATGTGAGA AAAATAAGCA 600
GGACACAATT ACAACTAAAA AATATATCTA AGCATTTGCA AAGGCGACAA TAAATTATTG 660
ACGCTTAACC TTTCCAGTTT ATAAGACTGG A

- (2) INFORMATION FOR SEQ ID NO:134:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 10987 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Genomic DNA
  - (ix) FEATURE
    - (A) NAME/KEY: coding sequence
    - (B) LOCATION: 229...10485
    - (D) OTHER INFORMATION: GenBank Accession No. U43746, BRCA2 gene

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
	CTCGGGTGTC					120
	GACCGGCGCG					180
	CTTATTTACC					240
	GGCCAACATT					300
	GTCTTAATTG					360
	AAGAATCTGA					420
	AACCATCTTA					480
	TGCCGCTGTA					540
	ATGTTCCCAA					600
	ATGATGTTTC					660
	GTACACATGT					720
TTTTCATACAAT	CAAAGTTTGT	GAAGGGTCGT	CAGACACCAA	AACATATTTC	TGAAAGTCTA	780
CCACCTCACC	TGGATCCTGA	TATCTCTTCG	TCAAGTTCTT	TAGCTACACC	ACCCACCCTT	840
A COUNCIE A COUC	TGCTCATAGT	CAGAAATGAA	GAAGCATCTG	AAACTGTATT	TCCTCATGAT	900
AGTICIACIO	ATGTGAAAAG	CHOARTOR	AATCATGATG	AAAGTCTGAA	GAAAAATGAT	960
	CTTCTGTGAC					1020
	AAACATCAGG					1080
	CAAATGTCCT					1140
	TTTCATTATG					1200
	CTAGGAAAAA					1260
ACTAGCAAGA	TGAAAGAAAA	AMITITOCAL	CTATCTCAACG	TCCAACCAAA	TGATACTGAT	1320
AAAAACCAAG	CAAATGTAGC	ACATCACAAC	CCCTTTCACA	GTGGAAGTGA	CAAAATCTCC	1380
CCATTAGATT	TACCGTCTTT	CCCCTCTCA	TCCTTTCAGA	TAACCCTTTC	AGGTCTAAAT	1440
AAGGAAGTTG	TGGAGAAAAT	ACCCCTATORA	CATATTTCTT	CATGTGACCA	ΔΔΤΔΤΤΤΤ	1500
GGAGCCCAGA	TATTAGACAC	ACCCCIAIIG	ACANACANAC	ATTTTTTTTAC	TTCAGAGAAT	1560
						1620
	GTATTTCTAG					1680
	GAGATGAAGA TATCTGGAAC					1740
AAGCAGGCAA	TATCTGGAAC	TICTCCAGIG	A COMMON A MC	CAACUUUUU	ACCTCATATC	1800
ATATTCAGAA	TAAGAGAATC ACTTTAAAAA	ACCTAAAGAG	ACTITICAAIG	CHAGIIIIC	AGGICATATG	1860
	AGAAGGAGGA					1920
GTTTGCTCAC	CACAGAATTC	CTCCTTATGT	A A CA A TO CA C	CTTTTATATIC	CACTTTCAAA	1980
GCCACCACCA	ATAAGTTTAT	TGTAGCTTTG	AAGAAIGCAG	CATTENTATA	ACCITIONA	2040
AAGAAAACAA	ACCAAAAATC	TTATGCTATA	A A CONCOUNT CA C	CCCACTTTCA	AGGAAAAAAA	2100
ATACCGAAAG	CACTTACATT	AGAACTAATT	AACIGIICAG	TATTCCATTC	TTCTCTCDAA	2160
	CACAGAATGA					2220
	GGAAATGTTC					2280
	ATAAAGAAGC					2340
GATCTTGATT	CTCTGTCATG	AAAAIGIAAI	CCACACTCTC	A A A A TCATCC	AAAAAGCAAA	2400
GAAGCTGATT	CTCTGTCATG	A CA COMOTTO	CCTCCACCAT	CTCACCCACT	ACAACATTCA	2460
AAAGTTTCAG	ATATAAAAGA	AGAGGICIIG	TCCCACAAAA	CTCTCTTTATA	TGATCATGAA	2520
AAAGTGGAAT	ACAGTGATAC	A A CONCOURA CON	TCCCAGAAAA	TTCTCTCAAAA	CCTAGTCATG	2580
AATGCCAGCA	CTCTTATTTT	AACTCCTACT	TCCAAGGAIG	TCAAACCTAA	CAATTATGAA	2640
ATTTCTAGAG	GCAAAGAATC	ATACAAAATG	TCAGACAAGC	A TO A A CATOT	ATGTGCTTTA	2700
TCTGATGTTG	AATTAACCAA	MAATATTCCC man comorumo	AIGGAAAAGA	AICAAGAIGI	AGTAGCATCA	2760
						2820
CCTTCAAGAA	AGGTACAATT	CAACCAAAAC	ACAAAICIAA	DAGIAAICCA DOTOTODADA	AAAAAATCAA	2880
GAAGAAACTA	CTTCAATTTC	AAAAATAACT	GICAAICCAG	CCAATAATCT	ACTTTTCTCA TGCTTTAGGA	2940
GACAATGAGA	ATAATTTTGT	P. A. C. P. C. C. C. C. C.	CTAAIGAAA	ACCAACACCAT	TTTTCAACAAC	3000
AATACTAAGG	AACTTCATGA	AACAGACTTG	ACTIGIGIAA	CARCCCAI	TTTCAAGAAC GTCAATTAAA	3060
TCTACCATGG	TITTATATGG	AGACACAGGT	GATAAACAAG	CAACCCAAGI CACCCAAGI	GCATATAAAA	3120
AAAGATTTTGG	TITATGTTCT	A A A TOCOCA C	X4C4444414	אטטאאאנטנא גאיימטאיימיימ	AATACCAGAA	3180
ATGACTCTAG	GTCAAGATTT	AAAATUGGAU	CONCECUTION	CTCCVVTTAC	AVIUCCUCUU	3240
AAAAATAATG	ATTACATGAA	CAAATGGGCA	. GGACICIIAG	ACCECHAIIIC ACCECHAIIIC	AAATCACAGT ACATAACATT	3300
TTTGGAGGTA	GCTTCAGAAC	AGCTTCAAAT	AAGGAAAICA	AGCICICIGA	ACAIAACAII	3300

```
AAGAAGAGCA AAATGTTCTT CAAAGATATT GAAGAACAAT ATCCTACTAG TTTAGCTTGT
GTTGAAATTG TAAATACCTT GGCATTAGAT AATCAAAAGA AACTGAGCAA GCCTCAGTCA
                                                                   3420
ATTAATACTG TATCTGCACA TTTACAGAGT AGTGTAGTTG TTTCTGATTG TAAAAATAGT
                                                                   3480
CATATAACCC CTCAGATGTT ATTTTCCAAG CAGGATTTTA ATTCAAACCA TAATTTAACA
CCTAGCCAAA AGGCAGAAAT TACAGAACTT TCTACTATAT TAGAAGAATC AGGAAGTCAG
                                                                   3600
TTTGAATTTA CTCAGTTTAG AAAACCAAGC TACATATTGC AGAAGAGTAC ATTTGAAGTG
CCTGAAAACC AGATGACTAT CTTAAAGACC ACTTCTGAGG AATGCAGAGA TGCTGATCTT
CATGTCATAA TGAATGCCCC ATCGATTGGT CAGGTAGACA GCAGCAAGCA ATTTGAAGGT
                                                                   3780
ACAGTTGAAA TTAAACGGAA GTTTGCTGGC CTGTTGAAAA ATGACTGTAA CAAAAGTGCT
                                                                    3840
TCTGGTTATT TAACAGATGA AAATGAAGTG GGGTTTAGGG GCTTTTATTC TGCTCATGGC
ACAAAACTGA ATGTTTCTAC TGAAGCTCTG CAAAAAGCTG TGAAACTGTT TAGTGATATT
                                                                   3960
GAGAATATTA GTGAGGAAAC TTCTGCAGAG GTACATCCAA TAAGTTTATC TTCAAGTAAA
                                                                   4020
TGTCATGATT CTGTTGTTTC AATGTTTAAG ATAGAAAATC ATAATGATAA AACTGTAAGT
                                                                   4080
GAAAAAAAA ATAAATGCCA ACTGATATTA CAAAATAATA TTGAAATGAC TACTGGCACT
TTTGTTGAAG AAATTACTGA AAATTACAAG AGAAATACTG AAAATGAAGA TAACAAATAT
                                                                   4200
ACTGCTGCCA GTAGAAATTC TCATAACTTA GAATTTGATG GCAGTGATTC AAGTAAAAAT
                                                                   4260
GATACTGTTT GTATTCATAA AGATGAAACG GACTTGCTAT TTACTGATCA GCACAACATA
TGTCTTAAAT TATCTGGCCA GTTTATGAAG GAGGGAAACA CTCAGATTAA AGAAGATTTG
                                                                    4380
TCAGATTTAA CTTTTTTGGA AGTTGCGAAA GCTCAAGAAG CATGTCATGG TAATACTTCA
                                                                    4440
AATAAAGAAC AGTTAACTGC TACTAAAACG GAGCAAAATA TAAAAGATTT TGAGACTTCT
GATACATTTT TTCAGACTGC AAGTGGGAAA AATATTAGTG TCGCCAAAGA GTCATTTAAT
                                                                    4560
AAAATTGTAA ATTTCTTTGA TCAGAAACCA GAAGAATTGC ATAACTTTTC CTTAAATTCT
                                                                    4620
GAATTACATT CTGACATAAG AAAGAACAAA ATGGACATTC TAAGTTATGA GGAAACAGAC
                                                                    4680
ATAGTTAAAC ACAAAATACT GAAAGAAAGT GTCCCAGTTG GTACTGGAAA TCAACTAGTG
ACCTTCCAGG GACAACCCGA ACGTGATGAA AAGATCAAAG AACCTACTCT GTTGGGTTTT
                                                                    4800
CATACAGCTA GCGGGAAAAA AGTTAAAATT GCAAAGGAAT CTTTGGACAA AGTGAAAAAC
                                                                    4860
CTTTTTGATG AAAAAGAGCA AGGTACTAGT GAAATCACCA GTTTTAGCCA TCAATGGGCA
AAGACCCTAA AGTACAGAGA GGCCTGTAAA GACCTTGAAT TAGCATGTGA GACCATTGAG
                                                                    4980
ATCACAGCTG CCCCAAAGTG TAAAGAAATG CAGAATTCTC TCAATAATGA TAAAAACCTT
                                                                   5040
GTTTCTATTG AGACTGTGGT GCCACCTAAG CTCTTAAGTG ATAATTTATG TAGACAAACT
                                                                    5100
GAAAATCTCA AAACATCAAA AAGTATCTTT TTGAAAGTTA AAGTACATGA AAATGTAGAA
                                                                    5160
AAAGAAACAG CAAAAAGTCC TGCAACTTGT TACACAAATC AGTCCCCTTA TTCAGTCATT
                                                                    5220
GAAAATTCAG CCTTAGCTTT TTACACAAGT TGTAGTAGAA AAACTTCTGT GAGTCAGACT
                                                                   5280
TCATTACTTG AAGCAAAAAA ATGGCTTAGA GAAGGAATAT TTGATGGTCA ACCAGAAAGA 5340
ATAAATACTG CAGATTATGT AGGAAATTAT TTGTATGAAA ATAATTCAAA CAGTACTATA
                                                                   5400
GCTGAAAATG ACAAAAATCA TCTCTCCGAA AAACAAGATA CTTATTTAAG TAACAGTAGC
                                                                   5460
ATGTCTAACA GCTATTCCTA CCATTCTGAT GAGGTATATA ATGATTCAGG ATATCTCTCA
                                                                    5520
AAAAATAAAC TTGATTCTGG TATTGAGCCA GTATTGAAGA ATGTTGAAGA TCAAAAAAAAC
ACTAGTTTTT CCAAAGTAAT ATCCAATGTA AAAGATGCAA ATGCATACCC ACAAACTGTA
                                                                    5640
AATGAAGATA TTTGCGTTGA GGAACTTGTG ACTAGCTCTT CACCCTGCAA AAATAAAAAT
                                                                   5700
GCAGCCATTA AATTGTCCAT ATCTAATAGT AATAATTTTG AGGTAGGGCC ACCTGCATTT
AGGATAGCCA GTGGTAAAAT CGTTTGTGTT TCACATGAAA CAATTAAAAA AGTGAAAGAC
                                                                  5820
ATATTTACAG ACAGTTTCAG TAAAGTAATT AAGGAAAACA ACGAGAATAA ATCAAAAATT 5880
TGCCAAACGA AAATTATGGC AGGTTGTTAC GAGGCATTGG ATGATTCAGA GGATATTCTT
                                                                    5940
CATAACTCTC TAGATAATGA TGAATGTAGC ACGCATTCAC ATAAGGTTTT TGCTGACATT
                                                                     6000
CAGAGTGAAG AAATTTTACA ACATAACCAA AATATGTCTG GATTGGAGAA AGTTTCTAAA
                                                                    6060
ATATCACCTT GTGATGTTAG TTTGGAAACT TCAGATATAT GTAAATGTAG TATAGGGAAG
                                                                     6120
CTTCATAAGT CAGTCTCATC TGCAAATACT TGTGGGATTT TTAGCACAGC AAGTGGAAAA
TCTGTCCAGG TATCAGATGC TTCATTACAA AACGCAAGAC AAGTGTTTTC TGAAATAGAA
                                                                    6240
GATAGTACCA AGCAAGTCTT TTCCAAAGTA TTGTTTAAAA GTAACGAACA TTCAGACCAG
                                                                    6300
CTCACAAGAG AAGAAAATAC TGCTATACGT ACTCCAGAAC ATTTAATATC CCAAAAAGGC
                                                                     6360
TTTTCATATA ATGTGGTAAA TTCATCTGCT TTCTCTGGAT TTAGTACAGC AAGTGGAAAG
CAAGTTTCCA TTTTAGAAAG TTCCTTACAC AAAGTTAAGG GAGTGTTAGA GGAATTTGAT
                                                                    6480
TTAATCAGAA CTGAGCATAG TCTTCACTAT TCACCTACGT CTAGACAAAA TGTATCAAAA
                                                                    6540
ATACTTCCTC GTGTTGATAA GAGAAACCCA GAGCACTGTG TAAACTCAGA AATGGAAAAA
                                                                  6600
ACCTGCAGTA AAGAATTTAA ATTATCAAAT AACTTAAATG TTGAAGGTGG TTCTTCAGAA
AATAATCACT CTATTAAAGT TTCTCCATAT CTCTCTCAAT TTCAACAAGA CAAACAACAG 6720
```

TTGGTATTAG	GAACCAAAGT	CTCACTTGTT	GAGAACATTC	ATGTTTTGGG	AAAAGAACAG	6780
GCTTCACCTA	AAAACGTAAA	AATGGAAATT	GGTAAAACTG	AAACTTTTTC	TGATGTTCCT	6840
GTGAAAACAA	ATATAGAAGT	TTGTTCTACT	TACTCCAAAG	ATTCAGAAAA	CTACTTTGAA	6900
ACAGAAGCAG	TAGAAATTGC	TAAAGCTTTT	ATGGAAGATG	ATGAACTGAC	AGATTCTAAA	6960
CTGCCAAGTC	ATGCCACACA	TTCTCTTTTT	ACATGTCCCG	AAAATGAGGA	AATGGTTTTG	7020
TCAAATTCAA	GAATTGGAAA	AAGAAGAGGA	GAGCCCCTTA	TCTTAGTGGG	AGAACCCTCA	7080
ATCAAAAGAA	ACTTATTAAA	TGAATTTGAC	AGGATAATAG	AAAATCAAGA	AAAATCCTTA	7140
AAGGCTTCAA	AAAGCACTCC	AGATGGCACA	ATAAAAGATC	GAAGATTGTT	TATGCATCAT	7200
GTTTCTTTAG	AGCCGATTAC	CTGTGTACCC	TTTCGCACAA	CTAAGGAACG	TCAAGAGATA	7260
	ATTTTACCGC					7320
	TGGAAAAATC					7380
	CAAGAAATGA					7440
	CACCTTTTAA					7500
	TGGAGGAAAA					7560
	AGATTAATGA					7620
	TAACTTTCAC					7680
	GAGATATACA					7740
	GCAGTCTGTA					7800
	GAGGCCAAGT					7860
	ATTGCATAAA					7920
	TTGGTAAGGA					7980
	TACCCTCCAA					8040
	CAGGTGTGGA					8100
	TATGGAAACT					8460
						8220
	GCCCAGAAAG					8280
	GAAGATCGGC					8340
	TCTGTGTTTC				TGAAACTTCT	8400
	CTAGTAGTGC				TACAGATGGG	
	TTAAGGCCCA					8460
	GTCAGAAGAT				TCCTGATGCC	8520
	TTGAAGCCCC					8580
	GGTATACCAA		TTTCCTGACC		TCCTCTGCCC	8640
	TTTTCAGTGA				TATTCAAAGA	8700
	TACAGTGGAT				TCGCAATGAA	8760
	AAAAGGAAGC					8820
	AAATTCAGGA					8880
	GTGCACTAAC					8940
	TGAAGAATGC					9000
CAGTTAAGAG	CCTTGAATAA	TCACAGGCAA	ATGTTGAATG	ATAAGAAACA	AGCTCAGATC	9060
	TTAGGAAGGC					9120
GATGTCACAA	CCGTGTGGAA	GTTGCGTATT	GTAAGCTATT	CAAAAAAAAGA	AAAAGATTCA	9180
GTTATACTGA	GTATTTGGCG	TCCATCATCA	GATTTATATT	CTCTGTTAAC	AGAAGGAAAG	9240
AGATACAGAA	TTTATCATCT	TGCAACTTCA	AAATCTAAAA	GTAAATCTGA	AAGAGCTAAC	9300
ATACAGTTAG	CAGCGACAAA	AAAAACTCAG	TATCAACAAC	TACCGGTTTC	AGATGAAATT	9360
TTATTTCAGA	TTTACCAGCC	ACGGGAGCCC	CTTCACTTCA	GCAAATTTTT	AGATCCAGAC	9420
					TGTGAAAAAA	9480
ACAGGACTTG	CCCCTTTCGT	CTATTTGTCA	GACGAATGTT	ACAATTTACT	GGCAATAAAG	9540
TTTTGGATAG	ACCTTAATGA	GGACATTATT	AAGCCTCATA	TGTTAATTGC	TGCAAGCAAC	9600
CTCCAGTGGC	GACCAGAATC	CAAATCAGGC	CTTCTTACTT	TATTTGCTGG	AGATTTTTCT	9660
GTGTTTTCTG	CTAGTCCAAA	AGAGGGCCAC	TTTCAAGAGA	CATTCAACAA	AATGAAAAAT	9720
ACTGTTGAGA	ATATTGACAT	ACTTTGCAAT	GAAGCAGAAA	ACAAGCTTAT	GCATATACTG	9780
CATGCAAATG	ATCCCAAGTG	GTCCACCCCA	ACTAAAGACT	GTACTTCAGG	GCCGTACACT	9840
GCTCAAATCA	TTCCTGGTAC	AGGAAACAAG	CTTCTGATGT	CTTCTCCTAA	TTGTGAGATA	9900
TATTATCAAA	GTCCTTTATC	ACTTTGTATG	GCCAAAAGGA	AGTCTGTTTC	CACACCTGTC	9960
TCAGCCCAGA	TGACTTCAAA	GTCTTGTAAA	GGGGAGAAAG	AGATTGATGA	CCAAAAGAAC	10020
TGCAAAAAGA	GAAGAGCCTT	GGATTTCTTG	AGTAGACTGC	CTTTACCTCC	ACCTGTTAGT	10080
CCCATTTGTA	CATTTGTTTC	TCCGGCTGCA	CAGAAGGCAT	TTCAGCCACC	AAGGAGTTGT	10141

GGCACCAAAT ACGAAACACC	CATAAAGAAA	AAAGAACTGA	ATTCTCCTCA	GATGACTCCA	10200
000	TTCTCTTTTG	GAAAGTAATT	CAATAGCTGA	CGAAGAACTT	10260
IIIAAAAAI totuttotutt	TCTTTTGTCT	GGTTCAACAG	GAGAAAAACA	ATTTATATCT	10320
OCHIIOMI MIMOOOM	TGCTCCCACC	AGTTCAGAAG	ATTATCTCAG	ACTGAAACGA	10380
GICHGIGHT CONSTRUCTIO	CAAAGAACAG	GAGAGTTCCC	AGGCCAGTAC	GGAAGAATGT	10440
COLLOTMONI CHICAGO		AAAAAATATA	TCTAAGCATT	TGCAAAGGCG	10500
0.10.1111111111111111111111111111111111	AACCTTTCCA	GTTTATAAGA	CTGGAATATA	ATTTCAAACC	10560
ACARIAARII RIIGHOOOTI	CACAATGAGA	AAAGAAATTA	GTTTCAAATT	TACCTCAGCG	10620
MCMCHILLING HOLLING	CGTTTTGCCC		TGGTATACTT	TTGCTTCAGT	10680
11101011110 000012222	GTAATTTATT	AACTAATCAA	GAAAAACATC	TTTGGCTGAG	10740
IGCATATOTT TERRITORIES	•		TGAGGTGGGA	GGAGTGCTTG	10800
CTCGGTGGCT CATGCCTGTA		CATAGGGAGA		TACGAAGAAA	10860
AGGCCAGGAG TTCAAGACCA		TCTTTGGATT	TGATCACTAC	AAGTATTATT	10920
AAAAAAAGG GGAAAAGAAA	ATCTTTTAAA			CTTTCAAATT	10980
TTACAATCAA CAAAATGGTC	ATCCAAACTC	AAACTTGAGA	AAATATCTTG	CITICAAATT	10987
GACACTA					10007